

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 30, 2006, 12:04:21 ; Search time 301 Seconds  
(without alignments)  
510.141 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897  
Sequence: 1 MAHAGRTGYDNRIVMKYIH.....WTDNGMGWDAFVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_treml.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	769.5	85.8	239	1 BCL2 HUMAN	P10415 homo sapien
2	767.5	85.6	229	1 BCL2 BOVIN	O02718 bos taurus
3	766.5	85.5	235	2 Q8I008 FELCA	Q8I008 felis silve
4	766.5	85.4	236	1 BCL2 RAT	P49950 rattus norv
5	765.5	85.3	239	2 Q75SV7 CANPA	Q75SV7 canis fami
6	757	84.4	236	2 Q4VBF6 MOUSE	Q4VBF6 mus musculu
7	757	84.4	236	2 Q7TSN8 RAT	Q7TSN8 rattus norv
8	757	84.4	236	2 Q8BQK4 MOUSE	Q8BQK4 mus musculu
9	752	83.8	236	1 BCL2 CRIGR	Q9JJV8 cricetulus
10	752	83.8	236	1 BCL2 MOUSE	P10417 mus musculu
11	752	83.8	236	2 Q923R6 CRILLO	Q923R6 cricetulus
12	749	83.5	236	2 Q6R755 CANPA	Q6R755 canis fami
13	712.5	79.4	185	2 Q8MJ81 BOVIN	Q8MJ81 bos taurus
14	710.5	79.2	233	1 BCL2 CHICK	Q00709 gallus gall
15	694	77.4	199	2 Q6NTH7 MOUSE	Q6NTH7 mus musculu
16	606	67.6	153	2 Q7YRB6 CANPA	Q7YRB6 canis fami
17	556	62.0	166	2 Q6R7E0 MESAU	Q6R7E0 mesocricetu
18	545	60.8	209	2 Q462R3 BOVIN	Q462R3 bos taurus
19	529	59.0	233	2 Q5C289 HUMAN	Q5C289 homo sapien
20	527	58.8	205	2 Q5TE64 HUMAN	Q5TE64 homo sapien
21	527	58.8	233	1 BCLX HUMAN	Q07817 homo sapien
22	527	58.8	233	2 Q5TE65 HUMAN	Q5TE65 homo sapien
23	527	58.8	233	2 Q8SQ42 FELCA	Q8SQ42 felis silve
24	527	58.8	233	2 Q9N1A2 PIG	Q9N1A2 sus scrofa
25	525	58.5	233	2 Q9M2S7 SHEEP	Q9M2S7 ovis aries
26	524	58.4	233	2 BCLX PIG	Q77737 sus scrofa
27	522	58.2	233	1 Q9MYW4 RABIT	Q9MYW4 oryctolagus
28	515	57.4	233	1 BCLX MOUSE	Q64373 mus musculu
29	511	57.0	233	2 Q5H2H3 MOUSE	Q5H2H3 mus musculu
30	511	57.0	233	2 BCLX RAT	P53563 rattus norv
31	509	56.7	233	1 BCLX RAT	

32 509 56.7 233 2 Q52KS0 RAT Q52KS0 rattus norv  
33 508 56.6 233 2 Q3T9W4 MOUSE Q3T9W4 mus musculu  
34 489 54.5 188 2 Q9H1R6 HUMAN Q9H1R6 homo sapien  
35 486 54.2 154 2 Q6LD89 BMURI Q6LD89 rattus ep.  
36 485 54.1 212 2 Q462R5 BOVIN Q462R5 bos taurus  
37 480 53.5 228 2 Q564A4 BRARE Q564A4 brachydanio  
38 476 53.1 188 2 Q9QWX2 MOUSE Q9QWX2 mus musculu  
39 475 53.0 235 2 Q35843 MOUSE Q35843 mus musculu  
40 475 53.0 284 2 Q7TS62 RAT Q7TS62 rattus norv  
41 473 52.7 217 2 Q9N335 MOUSE Q9N335 mus musculu  
42 459.5 51.2 159 2 Q4U2V0 PPASS Q4U2V0 lonchura st  
43 455.5 50.8 230 2 Q4U2V6 PPASS Q4U2V6 lonchura st  
44 449 50.1 181 2 Q5QP56 HUMAN Q5QP56 homo sapien  
45 445 49.6 229 1 BCLX\_CHICK Q07816 gallus gall

#### ALIGNMENTS

#### RESULT 1

ID BCL2 HUMAN STANDARD; PRT; 239 AA.  
AC P10415; P10416; Q13842; Q16197;  
DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.  
DT 01-APR-1993, sequence version 85.  
DE Apoptosis regulator Bcl-2.  
GN Name=BCL2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE (ISOFORMS ALPHA AND BETA).  
RX MEDLINE=86259760; PubMed=3523487;  
RA Tsujimoto Y., Croce C.M.;  
RT "Analysis of the structure, transcripts, and protein products of bcl-2, the gene involved in human follicular lymphoma.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
RN [2]  
RP SEQUENCE REVISION TO 96; 110 AND 237.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";  
RL Nucleic Acids Res. 20:4187-4192(1992).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=87002488; PubMed=2875799; DOI=10.1016/0092-8674(86)90362-4;  
RA Cleary M.L., Smith S.D., Sklar J.;  
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin transcript resulting from the t(14;18) translocation.";  
RL Cell 47:19-28(1986).  
RN [4]  
RP NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).  
RX MEDLINE=88196071; PubMed=2834197;  
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldman P., Korsmeyer S.J.;  
RT "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-Jg fusion gene in lymphoma.";  
RL EMBO J. 7:123-131(1988).  
RN [5]  
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANT THR-43.  
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;  
RT "NIH-SNPs, environmental genome project, NIH-S ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
RN [6]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND VARIANT SER-7.  
RX MEDLINE=88217344; PubMed=3285301;  
RA Hua C., Zorn S., Jensen J.P., Coupland R.W., Ko H.S., Wright J.J.,  
RA Bakhshi A.;  
RT "Consequences of the t(14;18) chromosomal translocation in follicular  
RT lymphoma: deregulated expression of a chimeric and mutated BCL-2  
RT gene";  
RL Oncogene Res. 2:263-275 (1988).  
RN [7]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulliahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [8]  
RP NUCLEOTIDE SEQUENCE OF 1-131 (ISOFORM ALPHA), AND VARIANTS NON-HODGKIN  
RP LYMPHOMA SER-59 AND ILE-93.  
RX MEDLINE=92096610; PubMed=1339299;  
RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
RT "Frequent incidence of somatic mutations in translocated BCL2  
RT oncogenes of non-Hodgkin's lymphomas";  
RL Blood 79:229-237 (1992).  
RN [9]  
RP SUBCELLULAR LOCATION  
RX MEDLINE=91066924; PubMed=2250705; DOI=10.1038/348334a0;  
RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
RT programmed cell death.";  
RL Nature 348:334-336 (1990).  
RN [10]  
RP MUTAGENESIS.  
RX MEDLINE=94239528; PubMed=8183370; DOI=10.1038/369321a0;  
RA Yin X.-M., Oltvai Z.N., Korsmeyer S.J.;  
RT "Bhl and BH2 domains of Bcl-2 are required for inhibition of apoptosis  
RT and heterodimerization with Bax";  
RL Nature 369:321-323 (1994).  
RN [11]  
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
RX MEDLINE=98057466; PubMed=9395403; DOI=10.1126/science.278.5345.1966;  
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
RA Ueno K., Hardwick J.M.;  
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases";  
RL Science 278:1966-1968 (1997).  
RN [12]  
RP INTERACTION WITH TP53BP2.  
RX MEDLINE=96251339; PubMed=8668206;  
RA Naumovski L., Cleary M.L.;  
RT "The p53-binding protein 53BP2 also interacts with Bcl2 and impedes  
RT cell cycle progression at G2/M";  
RL Mol. Cell. Biol. 16:3884-3892 (1996).  
RN [13]  
RP REVIEW ON PHOSPHORYLATION.  
RX MEDLINE=21260650; PubMed=11368354; DOI=10.1038/sj/leu/2402090;  
RA Ruvoilo P.P., Deng X., May W.S.;  
RT "Phosphorylation of Bcl2 and regulation of apoptosis";

RL Leukemia 15:515-522 (2001).  
RN [14]  
RP PHOSPHORYLATION BY ASK1/JNK1.  
RX MEDLINE=20036804; PubMed=10567572;  
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
RT protein kinase pathway normally activated at G(2)/M";  
RL Mol. Cell. Biol. 19:8469-8478 (1999).  
RN [15]  
RP INTERACTIONS WITH BBC3 AND BCL2L1.  
RX MEDLINE=21394643; PubMed=11463391; DOI=10.1016/S1097-2765(01)00213-1;  
RA Yu J., Zhang L., Huang P.M., Kinzler K.W., Vogelstein B.;  
RT "PUMA induces the rapid apoptosis of colorectal cancer cells";  
RL Mol. Cell 7:673-682 (2001).  
RN [16]  
RP INTERACTIONS WITH BNIP1.  
RX MEDLINE=22783925; PubMed=12901880; DOI=10.1016/S0006-291X(03)01387-1;  
RA Qiu W., Hu J., Guo M., Xu J., Li J., Yao G., Zhou X., Jiang H.,  
RA Zhang P., Shen L., Wan D., Gu J.;  
RT "BNIP1-2, a novel homologue of BNIP-2, interacts with Bcl-2 and  
RT Cdc42GAP in apoptosis";  
RL Biochem. Biophys. Res. Commun. 308:379-385 (2003).  
CC -I- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC -I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-X(L). Heterodimerization with BAX requires intact Bhl and BH2  
CC motifs, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1, RAP-1, TP53BP2, BBC3,  
CC BCL2L1 and BNIP1.  
CC -I- INTERACTION:  
CC Self: NbExp=1; IntAct=EBI-77694, EBI-77694;  
CC Q66P68-; NbExp=1; IntAct=EBI-77694, EBI-519932;  
CC Q29934:BAD; NbExp=3; IntAct=EBI-77694, EBI-700771;  
CC Q61337:Bad (xeno); NbExp=2; IntAct=EBI-77694, EBI-400328;  
CC Q16611:BAK1; NbExp=1; IntAct=EBI-77694, EBI-519866;  
CC Q07812:BAX; NbExp=2; IntAct=EBI-77694, EBI-516580;  
CC Q07813:Bax (xeno); NbExp=1; IntAct=EBI-77694, EBI-700711;  
CC Q9BXH1:BBC3; NbExp=2; IntAct=EBI-77694, EBI-519884;  
CC Q9BXH1-1:BBC3; NbExp=1; IntAct=EBI-77694, EBI-519891;  
CC Q9BXH1-2:BBC3; NbExp=1; IntAct=EBI-77694, EBI-519896;  
CC P51572:BCAP31; NbExp=2; IntAct=EBI-77694, EBI-77683;  
CC O43521:BCL2L1; NbExp=1; IntAct=EBI-77694, EBI-526406;  
CC O43521-2:BCL2L1; NbExp=1; IntAct=EBI-77694, EBI-526420;  
CC O43521-3:BCL2L1 (xeno); NbExp=1; IntAct=EBI-77694, EBI-526067;  
CC P59597:Bid; NbExp=2; IntAct=EBI-77694, EBI-519672;  
CC Q13323:Bik; NbExp=1; IntAct=EBI-77694, EBI-700794;  
CC Q91Z59:Bmf (xeno); NbExp=1; IntAct=EBI-77694, EBI-708032;  
CC -I- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=P10415-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=P10415-2; Sequence=VSP\_000512;  
CC -I- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
CC -I- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
CC for interaction with RAP-1.  
CC -I- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
CC The PM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 motif, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol

CC promoting further caspase activity.  
 CC -!- DISEASE: A chromosomal aberration involving BCL2 may be a cause of

Query Match 85.8%; Score 769.5; DB 1; Length 239;  
 Best Local Similarity 72.5%; Pred. No. 1.5e-64;  
 Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 45  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDGAAPGAPAPGPISSQPGHTPHDA 60

QY 46 GTE-----EVVHLALROAGDDFSRRYRGDPAEMSSQLH 79  
 DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLTLRQAGDDFSRRYRGDPAEMSSQLH 120

QY 80 LTPFTARGPATVVEELFRDGVNMGRIVAFPPFGGVMCVESVNRMSPLVDNIALWMTEY 139  
 DB 121 LTPFTARGPATVVEELFRDGVNMGRIVAFPPFGGVMCVESVNRMSPLVDNIALWMTEY 180

QY 140 LNRHLHTWIQDNGGDAFVELYGPMSR 166  
 DB 181 LNRHLHTWIQDNGGDAFVELYGPMSR 207

RESULT 2  
 BCL2 BOVIN STANDARD; PRT; 229 AA.

AC Q02718;  
 DT 26-SEP-2001, integrated into UniProtKB/Swiss-Prot.  
 DT 01-JUL-1997, sequence version 1.  
 DT 07-MAR-2006, entry version 50.

DE Apoptosis regulator Bcl-2.  
 GN Name=BCL2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 -OX NCBI\_TaxID=9913;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [MRNA].  
 RC STRAIN=Holstein; TISSUE=Thymus;  
 RX MEDLINE=98162580; PubMed=9501036; DOI=10.1006/viro.1998.9029;  
 RA Reyes R.A., Cockerell G.L.;  
 RT "Increased ratio of bcl-2/bax expression is associated with bovine  
 RT leukemia virus-induced leukemogenesis in cattle.";  
 RL Virology 242:184-192(1998).

CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1) (By similarity).

CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC motifs, and is necessary for anti-apoptotic activity. Also  
 CC interacts with APAF-1, RAP-1, TP53BP2, BBC3, BCL2L1 and BNIP1 (By  
 CC similarity).

CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).

CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
 CC for interaction with RAP-1 (By similarity).

CC -!- PTM: Phosphorylation/dephosphorylation on Ser-63 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-63 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle (By similarity). In  
 CC the absence of growth factors, Bcl2 appears to be phosphorylated  
 CC by other protein kinases such as ERKs and stress-activated  
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 CC similarity).

CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 motif, has pro-apoptotic

CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.

CC -----  
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 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----

CC EMBL; U92434; AAB53319.1; -; mRNA.  
 CC HSSP; P10415; IGJH.  
 DR InterPro; IPR013278; Apop reg Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF00115; Bcl2 antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR PRINTS; PR01863; APOFREGBCL2.  
 DR PRINTS; PR01862; BCL2FAMILY.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 DR Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 KW Nuclear protein; Phosphorylation; Transmembrane.  
 FT CHAIN 1 229 Apoptosis regulator Bcl-2.  
 FT /FTID=PRO\_0000143046.

FT TRANSMEM 202 223 Potential.  
 FT MOTIF 10 30 BH4.  
 FT MOTIF 83 97 BH3.  
 FT MOTIF 126 145 BH1.  
 FT MOTIF 177 192 BH2.  
 FT COMPIAS 64 68 Poly-Pro.  
 FT COMPIAS 69 72 Poly-Ala.  
 FT SITE 34 35 Cleavage (by caspases) (By similarity).  
 FT MOD\_RES 63 63 Phosphoserine (by PKC) (By similarity).  
 SQ SEQUENCE 229 AA; 25100 MW; AD1DD0AF98FF1D CRC64;

Query Match 85.6%; Score 767.5; DB 1; Length 229;  
 Best Local Similarity 76.1%; Pred. No. 2.3e-64;  
 Matches 150; Conservative 2; Mismatches 14; Indels 31; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 45  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDAGAPGAPAPGPISSQPGHTPAPS 60

QY 46 GTE-----SEVVHLALROAGDDFSRRYRGDPAEMSSQLHPTFTARGRF 89  
 DB 61 RTPSPPPAAAAGPAPSPVPPVHLTLRQAGDDFSRRYRGDPAEMSSQLHPTFTARGRF 120

QY 90 ATVVEELRDGVNMGRIVAFPPFGGVMCVESVNRMSPLVDNIALWMTEYLNRLHTWIQ 149  
 DB 121 ATVVEELFRDGVNMGRIVAFPPFGGVMCVESVNRMSPLVDNIALWMTEYLNRLHTWIQ 180

QY 150 DNGGWDADFVELYGPMSR 166  
 DB 181 DNGGWDADFVELYGPMSR 197

RESULT 3  
 Q81008 FELCA  
 ID Q81008\_FELCA PRELIMINARY; PRT; 235 AA.  
 AC Q81008;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-MAR-2006, entry version 16.

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DE Bcl-2 protein.
GN Name=bcl-2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15893350; DOI=10.1016/j.rvec.2005.03.001;
RA Sano J., Nagafuchi S., Yamazaki J., Oguma K., Hasegawa A.;
RT "Effect of anticancer drugs on the expression of Bcl-2 and Bcl-xL
RL genes in the feline T-cell leukemia cell line.";
Res. Vet. Sci. 79:197-201(2005).
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DR EMBL; AB096611; BAC241136.1; -; mRNA.
DR HSPG; P10415; IGJH.
DR SMR; Q81008; 40-203.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR013278; Apop_reg_Bcl2.
DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2-reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PIRSF; PIRSF00115; Bcl2 antiapop; 1.
DR PIRSF; PIRSF001714; Bcl2 apop_reg; 1.
DR PRINTS; PR01863; APOPREGBCL2.
DR PRINTS; PR01862; BCL2FAMILY.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRfam; TIGR00865; bcl-2; 1.
DR PROSITE; PS00662; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS00663; BH4; 1.
DR PROSITE; PS00663; BH4; 1.
SQ SEQUENCE 235 AA; 25621 MW; 2320B57C96B64548 CRC64;

Query Match 85.5%; Score 766.5; DB 2; Length 235;
Best Local Similarity 73.4%; Pred No. 2,9e-64;
Matches 149; Conservative 3; Mismatches 14; Indels 37; Gaps 2;

QY 1 MAHAGRTGYDNRREIYKVIHYKLSQRYEWADG-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNRREIYKVIHYELPQRYEWADGAGAAPGAAAPGIFFSQPGRTTAPA 60
QY 46 GTE-----SEVHLALROAGDDFSRRYRGDFAEWSSQLHLTPF 83
DB 61 RTSPPPPPVAPAAAAAAGPALSPPVPHVLTLRQAGDDFSRRYRDRDFAEWSSQLHLTPF 120
QY 84 TARGFATVVEELPRDGNWGRIVAFEFEGGVMCVESPLVDNIALWMTTEYLNHR 143
DB 121 TARGFATVVEELPRDGNWGRIVAFEFEGGVMCVESPLVDNIALWMTTEYLNHR 180
QY 144 LHTWIQDNGGWDFAVELYGPSMR 166
DB 181 LHTWIQDNGGWDFAVELYGPSNQ 203

RESULT 4
BCL2 RAT
ID BCL2 RAT STANDARD; PRT; 236 AA.
AC P49550; Q62837; Q64032;
DT 01-OCT-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 2.
DT 07-MAR-2006, entry version 47.
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DE Apoptosis regulator Bcl-2.
GN Name=Bcl2; Synonyms=Bcl-2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX TISSUE=Brain;
MEDLINE=94193015; PubMed=8144041; DOI=10.1016/0378-1119(94)90561-4;
RA Sato T., Irie S., Krajewski S., Reed J.C.;
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
RL Gene 140:291-292(1994).
CC [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX STRAIN=Sprague-Dawley; TISSUE=Ovary;
MEDLINE=95129487; PubMed=7828536; DOI=10.1210/en.136.1.232;
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
cell apoptosis is associated with decreased bax and constitutive bcl-2
and bcl-xlong messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
CC [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 19-172.
RX MEDLINE=95059917; PubMed=7969891; DOI=10.1016/0306-4522(94)90069-8;
RA Castrén E., Ohga Y., Berzaghi M.P., Tzimagiorgis G., Thoenen H.,
RA Lindholm D.;
RT "bcl-2 messenger RNA is localized in neurons of the developing and
adult rat brain.";
RL Neuroscience 61:165-177(1994).
CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems
including factor-dependent lymphohematopoietic and neural cells.
Regulates cell death by controlling the mitochondrial membrane
permeability. Appears to function in a feedback loop system with
caspases. Inhibits caspase activity either by preventing the
release of cytochrome c from the mitochondria and/or by binding to
the apoptosis-activating factor (APAF-1).
-1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2
motifs, and is necessary for anti-apoptotic activity. Also
interacts with APAF-1, RAF-1, TP53BP2, BIRC3, BCL2L1 and BNIP1 (By
similarity).
-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
membrane of the nuclear envelope and the endoplasmic reticulum.
-1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with
highest levels in reproductive tissues. In the adult brain,
expression is localized in mitral cells of the olfactory bulb,
granule and pyramidal neurons of hippocampus, pontine nuclei,
cerebellar granule neurons, and in ependymal cells. In prenatal
brain, expression is higher and localized in the neuroepithelium
and in the cortical plate.
-1- DOMAIN: The BH4 motif is required for anti-apoptotic activity and
for interaction with RAF-1 (By similarity).
-1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
anti-apoptotic activity. Growth factor-stimulated phosphorylation
on Ser-70 by PKC is required for the anti-apoptosis activity and
occurs during the G2/M phase of the cell cycle. In the absence of
growth factors, Bcl2 appears to be phosphorylated by other protein
kinases such as ERKs and stress-activated kinases.
-1- PTM: Proteolytically cleaved by caspases during apoptosis. The
cleaved protein, lacking the BH4 motif, has pro-apoptotic
activity, causes the release of cytochrome c into the cytosol
promoting further caspase activity (By similarity).
-1- SIMILARITY: Belongs to the Bcl-2 family.
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CC -----
DR EMBL; L14680; AAA53662.1; -; mRNA.
DR EMBL; U34964; AAA77687.1; -; mRNA.
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DR EMBL; S74122; -, NOT\_ANNOTATED\_CDS; mRNA.  
 DR PIR; I53744; I53744.  
 DR PIR; I67432; I67432.  
 DR HSSP; P10415; LGJH.  
 DR SMR; P49950; 41-204.  
 DR Ensemble; ENSRNOG00000002791; Rattus norvegicus.  
 DR RGD; 2199; Bcl2.  
 DR GO; GO:0006916; P:anti-apoptosis; IDA.  
 DR GO; GO:0006915; P:apoptosis; TAS.  
 DR InterPro; IPR013278; Apopt reg Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2 family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF500115; Bcl2 antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR PRINTS; PRO1863; APOREGBCL2.  
 DR PRINTS; PRO1862; BCL2FAMILY.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM0265; BH4; 1.  
 DR TIGRFS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 DR PROSITE; PS50063; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 KW Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 Nuclear protein; Phosphorylation; Transmembrane.  
 FT CHAIN 1 236  
 /FTID-PRO 0000143050.  
 FT TRANSMEM 209 230  
 FT MOTIF 10 30  
 FT MOTIF 90 104  
 FT MOTIF 133 152  
 FT MOTIF 184 199  
 FT SITE 34 35  
 Cleavage (by caspases) (By similarity).  
 FT MOD\_RES 70 70  
 Phosphoserine (by PKC) (By similarity).  
 FT CONFLICT 42 42  
 A -> R (in Ref. 2).  
 FT CONFLICT 157 157  
 E -> G (in Ref. 1).  
 FT CONFLICT 164 164  
 S -> Y (in Ref. 2).  
 FT CONFLICT 212 212  
 L -> Q (in Ref. 2).  
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Query Match 85.4%; Score 766; DB 1; Length 236;  
 Best Local Similarity 73.5%; Pred. No. 3.3e-64;  
 Matches 150; Conservative 3; Mismatches 13; Indels 38; Gaps 2;  
 QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDD-----VEENRTEA 43  
 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDD-----VEENRTEA 60  
 QY 44 PEGTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLHLTP 82  
 DB 61 VHRDARTSPRLPLVANAGPALSPVPVPHLTLRAGDDFSRRYRGDFAEMSSQLHLTP 120  
 QY 83 FTARGFATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALMWTLEYLNR 142  
 DB 121 FTARGFATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALMWTLEYLNR 180  
 QY 143 HLHTWIQDNGWDFAVELYGPSMR 166  
 DB 181 HLHTWIQDNGWDFAVELYGPSMR 204

RESULT 5  
 Q75SV7 CANFA  
 ID Q75SV7 CANFA PRELIMINARY; PRT; 239 AA.  
 AC Q75SV7;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Bcl-2 protein.  
 GN Name=bcl-2;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 NCBI\_TaxID=9615;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sano J., Yamazaki J., Nagafuchi S., Kano R., Hasegawa A.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
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 CC  
 CC EMBL; AB154172; BAD05044.1; -; mRNA.  
 DR HSSP; P53563; IAF3.  
 DR SMR; Q75SV7; 44-207.  
 DR Ensemble; ENSCAFG00000000068; Canis familiaris.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR013278; Apop\_reg\_Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF500115; Bcl2 antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM0265; BH4; 1.  
 DR TIGRFS; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 DR PROSITE; PS50063; BH4\_1; 1.  
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 Query Match 85.3%; Score 765.5; DB 2; Length 239;  
 Best Local Similarity 72.0%; Pred. No. 3.7e-64;  
 Matches 149; Conservative 4; Mismatches 13; Indels 41; Gaps 2;  
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 DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 60  
 QY 46 GTE-----SEVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
 DB 61 RTSPPPPPAPAAAAAADAAGAPSPVPVPHLTLRAGDDFSRRYRGDFAEMSSQLH 120  
 QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALMWTLEY 139  
 DB 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGGVMCVESVNREMSPLVDNIALMWTLEY 180  
 QY 140 LNRHLHTWIQDNGWDFAVELYGPSMR 166  
 DB 181 LNRHLHTWIQDNGWDFAVELYGPSMR 207  
 RESULT 6  
 Q4VBF6 MOUSE  
 ID Q4VBF6 MOUSE PRELIMINARY; PRT; 236 AA.  
 AC Q4VBF6;  
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE Bcl2 protein.

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GN Name=Bcl2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alcehul S.F., Zeeberg B., Bueow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Olfactory epithelium;
RC NIH MGC Project;
RG Submitted (MAY-2005) to the EMBL/GenBank/DBSJ databases.
RL
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CC
CC
DR EMBL; BC095964; AAH95964.1; -; mRNA.
DR SMR; QAVB6; 41-204
DR MGI; MGI:88138; Bcl2.
DR GO; GO:0005829; Cytozol; IDA.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR GO; GO:0005515; P:protein binding; IPT.
DR GO; GO:0006916; P:anti-apoptosis; IGI.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR GO; GO:0006916; P:apoptosis; IDA.
DR GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.
DR InterPro; IPR013278; Apop_reg_Bcl2.
DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH4.
DR InterPro; IPR003093; Bcl2_family.
DR InterPro; IPR002475; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
DR SMART; SM00337; BCL; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS0063; BH4_2; 1.
DR SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
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Query Match 84.4%; Score 757; DB 2; Length 236;
Best Local Similarity 72.2%; Pred. No. 2.3e-63;
Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;
CC
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Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAAGDDVVENRTEAPEGT-----ES 49
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Qy 50 E-----VVHLALRQAGDDFSRRYRGDFAEWSSQ 77
Db 56 NPMPAVHRDMAARTSPRLPLVATAGPALSPPVPVVLTLRAGDDFSRRYRRDFAEWSSQ 115
Qy 78 LHTPTTARGRTATVVEELFRDGVNMGRIVAFPEFGVGMCVESVNRMSPLVDNIALWMT 137
Db 116 LHTPTTARGRTATVVEELFRDGVNMGRIVAFPEFGVGMCVESVNRMSPLVDNIALWMT 175
Qy 138 EYLNRLHHTWIQDNGGWDFAFVELYGPMSR 166
Db 176 EYLNRLHHTWIQDNGGWDFAFVELYGPMSR 204
RESULT 7
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ID Q7TSN8 RAT AC Q7TSN8;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Bcl2-like protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Wistar;
RC Tanaka T., Nangaku M.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.
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CC
CC
DR EMBL; AF512835; AAP47159.1; -; mRNA.
DR HSSP; P10415; 1GJH.
DR SMR; Q7TSN8; 41-204.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
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DR InterPro; IPR012238; Bcl2_apop_reg.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; Bcl2_family.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR PIRSF; PIRSF00115; Bcl2_antiapop; 1.
DR PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4_1; 1.
DR PROSITE; PS0063; BH4_2; 1.
DR SEQUENCE 236 AA; 26407 MW; 80FDCFE78C735092 CRC64;
SQ
Query Match 84.4%; Score 757; DB 2; Length 236;
Best Local Similarity 72.2%; Pred. No. 2.3e-63;
Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;
Qy 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAAGDDVVENRTEAPEGT-----ES 49
Db 1 MAQAGRTGYDNREIVMKYIHYKLSQGYEWDAAGD-----ADAAPLGAAPTGGIFSFPES 55
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 QY 78 LHLTPPTARGATVVEELFRDGVNNGRIVAFEFGGVCMVSNREMSPLVDNIALWMT 137  
 DB 116 LHLTPPTARGATVVEELFRDGVNNGRIVAFEFGGVCMVSNREMSPLVDNIALWMT 175  
 QY 138 EYLNRLHLTWIQDNGWDAFVELYGPMSR 166  
 DB 176 EYLNRLHLTWIQDNGWDAFVELYGPMSR 204  
 RESULT 8  
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 ID Q8BQK4 MOUSE PRELIMINARY; PRT; 236 AA.  
 AC Q8BQK4  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 22.  
 DE 7 days embryo whole body cDNA, RIKEN full-length enriched library,  
 DE clone:C430015F12 product:B-cell leukemia/lymphoma 2, full insert  
 DE sequence.  
 GN Name=Bcl2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole body; STRAIN=C57BL/6J;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakayama H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlandini V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrosky N., Piazza S., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugtara K., Sultana R., Takenaka Y., Taki K.,  
 RA Tamaoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki K., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,

RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=12466851; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konggaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi E., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Whole body;  
 RX MEDLINE=21085860; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.





activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity.  
 -!- SIMILARITY: Belongs to the Bcl-2 family.  
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 EMBL; AJ271720; CAB92245.1; -, mRNA.  
 PIR; JC7383; JC7383.  
 HSP; P10415; IGJH.  
 SMR; Q9JUV8; 41-204.  
 InterPro; IPR013278; Apop\_reg\_Bcl2.  
 InterPro; IPR012238; Bcl2\_apop\_reg.  
 InterPro; IPR000712; Bcl2\_BH.  
 InterPro; IPR003093; Bcl2\_BH4.  
 InterPro; IPR002475; Bcl2\_family.  
 InterPro; IPR004725; Bcl2\_reg.  
 Pfam; PF00452; Bcl-2; 1.  
 Pfam; PF02180; BH4; 1.  
 PIRSF; PIRSF00115; Bcl2\_antiapop; 1.  
 PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
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 PRINTS; PR01862; BCL2FAMILY.  
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 SMART; SMO0265; BH4; 1.  
 TIGRFAMS; TIGR00865; bcl-2; 1.  
 PROSITE; PS50062; BCL2\_FAMILY; 1.  
 PROSITE; PS01080; BH1; 1.  
 PROSITE; PS01259; BH2; 1.  
 PROSITE; PS01259; BH3; 1.  
 PROSITE; PS01260; BH4; 1.  
 PROSITE; PS50063; BH4\_2; 1.  
 \*KW Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 \*KW Nuclear protein; Phosphorylation; Transmembrane; Bcl-2.  
 FT CHAIN 1 236 Apoptosis regulator Bcl-2.  
 FT FTID=PRO.0000143047.  
 FT TRANSMEM 209 230 Potential.  
 FT MOTIF 10 30 BH4.  
 FT MOTIF 90 104 BH3.  
 FT MOTIF 133 152 BH1.  
 FT MOTIF 184 199 BH2.  
 FT SITE 64 65 Cleavage (by caspase-3 and caspase-9).  
 FT MOD\_RES 70 70 Phosphoserine (by PKC) (By similarity).  
 SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF337228 CRC64;  
 Query Match 83.8%; Score 752; DB 1; Length 236;  
 Best Local Similarity 72.5%; Pred. No. 6.9e-63;  
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 QY 1 MAHAGRTGYDNRIVVMKYIHYKLSQRYEWDAGD-----DVEENRTEA 43  
 DB 1 MAQAGRTGYDNRIVVMKYIHYKLSQRYEWDGVDAAPIGAAPTGIQFSQPESNPTPA 60  
 QY 44 PE-----GTESEVVHLALRQAGDDFSRRYRGDFAEMSSQLHLTP 82  
 DB 61 VHRDMAARTSLRPIVATTGPTLSPPVPPVHLLTRAGDDFSRRYRDFAEMSSQLHLTP 120  
 QY 83 FTARGFATVVEELFRDGVNMGRIIVAFPPGGVCMVSNREMSPLVDNIALMTTYLNR 142  
 DB 121 FTARGFATVVEELFRDGVNMGRIIVAFPPGGVCMVSNREMSPLVDNIALMTTYLNR 180  
 QY 143 HLHTWIQDNGGWDFAVELYGPSNR 166  
 DB 181 HLHTWIQDNGGWDFAVELYGPSVR 204  
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 ID BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 AC P10417; P10418;  
 DT 01-JUL-1989, integrated into UniProtKB/Swiss-Prot.  
 DT 01-APR-1993, sequence version 2.  
 DT 07-MAR-2006, entry version 63.

DE Apoptosis regulator Bcl-2.  
 GN Name=Bcl2; Synonyms=Bcl-2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
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 RC STRAIN=BALB/c; TISSUE=Liver;  
 RX MEDLINE=87187643; PubMed=302455; DOI=10.1016/0092-8674(87)90448-X;  
 RA Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of bcl-2: structure and expression of the murine  
 gene homologous to the human gene involved in follicular lymphoma.";  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP SEQUENCE REVISION TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 in a variety of tissues including lymphoid and neuronal organs in  
 adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
 RX MEDLINE=97277291; PubMed=9115213; DOI=10.1074/jbc.272.18.11671;  
 RA Ito T., Deng X., Carr B., May W.S. Jr.;  
 RT "Bcl-2 phosphorylation required for anti-apoptosis function.";  
 RL J. Biol. Chem. 272:11671-11673(1997).  
 RN [4]  
 RP DEPHOSPHORYLATION BY PP2A.  
 RX MEDLINE=99069407; PubMed=9852076; DOI=10.1074/jbc.273.51.34157;  
 RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;  
 RT "Reversible phosphorylation of Bcl2 following interleukin 3 or  
 bryostatins 1 is mediated by direct interaction with protein  
 phosphatase 2A\*";  
 RL J. Biol. Chem. 273:34157-34163(1998).  
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 permeability. Appears to function in a feedback loop system with  
 caspases. Inhibits caspase activity either by preventing the  
 release of cytochrome c from the mitochondria and/or by binding to  
 the apoptosis-activating factor (APAF-1).  
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2  
 motifs, and is necessary for anti-apoptotic activity. Also  
 interacts with APAF-1, RAF-1, TP53BP2, BIRC3, BCL2L1 and BNIP1 (By  
 similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC ISOID=P10417-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC ISOID=P10417-2; Sequence=VSP\_000513;  
 CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
 CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
 for interaction with RAF-1.  
 CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 on Ser-70 by PKC is required for the anti-apoptosis activity and  
 occurs during the G2/M phase of the cell cycle. In the absence of  
 growth factors, Bcl2 appears to be phosphorylated by other protein  
 kinases such as ERKs and stress-activated kinases.  
 CC Dephosphorylated by protein phosphatase 2A (PP2A).  
 CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 cleaved protein, lacking the BH4 motif, has pro-apoptotic  
 activity, causes the release of cytochrome c into the cytosol  
 promoting further caspase activity.  
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.  
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CC EMBL; L31532; AAA37282.1; -; Genomic DNA.
CC EMBL; M16506; AAA37282.1; JOINED; Genomic DNA.
CC EMBL; M16506; AAA37281.1; -; Genomic DNA.
CC PIR; B25960; TMSB1.
CC HSSP; P10415; IGJH.
CC SMR; P10417; 41-204.
CC Ensembl; ENSMUSG0000057329; Mus musculus.
CC MGI; MGI:88138; Bcl2.
CC Reactome; P10417; -.
CC GO; GO:0005829; C:cytosol; IDA.
CC GO; GO:0005739; C:mitochondrion; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006916; P:anti-apoptosis; IDA.
CC GO; GO:0006915; P:apoptosis; IDA.
CC GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.
CC InterPro; IPR013278; Apop_reg_Bcl2.
CC InterPro; IPR012238; Bcl2_apop_reg.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; Bcl2_BH4.
CC InterPro; IPR002475; BCL2_FAMILY.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC PIRSF; PIRSF00115; Bcl2_antiapop; 1.
CC PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
CC PRINTS; PR01863; APOREGHC12.
CC PRINTS; PR01862; BCL2_FAMILY.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS00062; BCL2_FAMILY; 1.
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CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4; 1.
CC PROSITE; PS0063; BH4-2; 1.
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KW Apoptosis; Phosphorylation; Transmembrane.
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FT MOTIF 10 30
FT MOTIF 90 104
FT MOTIF 133 152
FT MOTIF 184 199
FT SITE 34 35
FT MOD_RES 70 70
FT VARSPIC 193 236
FT DAFVELYGFMSRPLDFSLSLKTLTLLSLALVGCITLGLAYL
FT GHK -> VGACLIVE (in isoform Beta).
FT /FTId=VSP_000513.
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QY 50 E-----VVHLALRQAGDDFSRRYRGDFAEMSSQ 77
DB 56 NMPAVHREMAARTSPRLVATAGPASPVPVPCVHLTLRRAGDDFSRRYRDFAEMSSQ 115
QY 78 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT 137
DB 116 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT 175
QY 138 EYLNRLHTWTIQDNGGDAFVELYGFMSR 166
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Db 176 EYLNRLHTWTIQDNGGDAFVELYGFMSR 204
RESULT 11
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AC Q923R6
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE B-cell lymphoma protein 2.
GN Name=bcl2;
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Cricetinae; Cricetus.
OX NCBI_TaxID=10030;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lai D.-Z., Chen W., Wang H.T.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC EMBL; AF040339; AAK92201.1; -; mRNA.
CC HSSP; P10415; IGJH.
CC SMR; Q923R6; 41-204.
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CC GO; GO:0042981; P:regulation of apoptosis; IEA.
CC InterPro; IPR013278; Apop_reg_Bcl2.
CC InterPro; IPR012238; Bcl2_apop_reg.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; BCL2_FAMILY.
CC InterPro; IPR002475; BCL2_FAMILY.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC PIRSF; PIRSF00115; Bcl2_antiapop; 1.
CC PIRSF; PIRSF001714; Bcl2_apop_reg; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS00062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4; 1.
CC PROSITE; PS0063; BH4-2; 1.
CC PROSITE; PS0063; BH4-2; 1.
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Query Match 83.8%; Score 752; DB 2; Length 236;
Best Local Similarity 72.5%; Pred. No. 6.9e-63;
Matches 148; Conservative 2; Mismatches 16; Indels 38; Gaps 2;

QY 1 MAHAGRTGYNREIYMKYIHYKLSQGYEWDAGD-----DVEENRTEA 43
DB 1 MAQAGRTGYNREIYMKYIHYKLSQGYEWDAGD-----DVEENRTEA 60
QY 44 PE-----GTESEVHLALRQAGDDFSRRYRGDFAEMSSQHLTP 82
DB 61 VHRDMAARTSPRLVATVATGPTLSPVPVPCVHLTLRRAGDDFSRRYRDFAEMSSQHLTP 120
QY 83 FTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT EYLNRL 142
DB 121 FTARGFATVVEELFRDGVNMGRIVAFPEFGVNCVSVNREMSPLVDNIALMWT EYLNRL 180
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DB 181 HLHTWTIQDNGGDAFVELYGFMSR 204
RESULT 12
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Q6R755 CANFA PRELIMINARY; PRT; 236 AA.  
 ID Q6R755; AC Q6R755;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE Bcl-2.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 OC Canis.  
 NCBI\_TaxID=9615;  
 RN NUCLEOTIDE SEQUENCE.  
 [1]  
 RA Chien M.B., London C.A., Jones C.S.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
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 CC  
 DR EMBL; AY509563; AAR92491.1; -; mRNA.  
 DR HSSP; P53563; IAF3.  
 DR SMR; Q6R755; 41-204.  
 DR Ensembl; ENSCARG0000000068; Canis familiaris.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR013278; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR012238; Apop reg Bcl2.  
 DR InterPro; IPR000712; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR InterPro; IPR004725; BCL2\_reg.  
 DR Pfam; PF0452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF500115; Bcl2 antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRfams; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4; 1.  
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 DB 1 MAAGRTGYDNRREIVMKYHYKLSQRYEWDGVDAAFLGAAPTFGIFSFQPSNPTPA 60  
 QY 44 PE-----GTESEVHLALRQAGDDFSRRYRGDFAEMSSQLHLTP 82  
 DB 61 VHRDMAARTSPLRPIVATTPTLSPVPVHLLTRAGDDFSRRYRRDFAEMSSQLHLTP 120  
 QY 83 FTARGRFATVVEELFRDGVNWRGRIVAFFFGVCMCVSNRMSPLVDNIALMTTEYLNR 142  
 DB 121 FTARGRFATVVEELFRDGVNWRGRIVAFFFGVCMCVSNRMSPLVDNIALMTTEYLNR 180  
 QY 143 HLHTWIQDNGGWDFAVELYGPSMR 166  
 DB 181 HLHTWIQDNGGWDFAVELYGPSMTQ 204  
 RESULT 13  
 Q8MJ81\_BOVIN PRELIMINARY; PRT; 185 AA.  
 ID Q8MJ81\_BOVIN  
 AC Q8MJ81;  
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE Bcl2 protein (Fragment).  
 GN Name=bcl2;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN NUCLEOTIDE SEQUENCE.  
 [1]  
 RA STRAIN=Jersey;  
 RX MEDLINE=22542224; PubMed=12655025; DOI=10.1093/nar/gng037;  
 RT Krebs S., Medugorac I., Seichter D., Forster M.;  
 RL "RNaseCut: a MALDI mass spectrometry-based method for SNP discovery."; Nucleic Acids Res. 31:E37-E37(2003).  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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 CC  
 DR EMBL; AF515848; AAN03862.1; -; Genomic\_DNA.  
 DR HSSP; P10415; IGJH.  
 DR Ensembl; ENSBTAG00000019302; Bos taurus.  
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.  
 DR InterPro; IPR013278; Apop reg Bcl2.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; BCL2\_family.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 DR NON\_TER 185  
 FT SEQUENCE 185 AA; 20260 MW; 8FA829629553C65F CRC64;  
 SQ  
 Query Match 79.4%; Score 712.5; DB 2; Length 185;  
 Best Local Similarity 75.1%; Pred. No. 2.9e-59;  
 Matches 139; Conservative 2; Mismatches 13; Indels 31; Gaps 2;  
 QY 1 MAHAGTGYDNRREIVMKYHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
 DB 1 MAHAGTGYDNRREIVMKYHYKLSQRYEWDAGAGAAPGAPGILSSQFGRTTAPS 60  
 QY 46 GTE-----SEVHLLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRF 89  
 DB 61 RTSPPPPPAAAGAPAPSPVPVHLLTRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGRF 120  
 QY 90 ATTVVEELFRDGVNWRGRIVAFFFGVCMCVSNRMSPLVDNIALMTTEYLNRHLHTWIQ 149  
 DB 121 ATTVVEELFRDGVNWRGRIVAFFFGVCMCVSNRMSPLVDNIALMTTEYLNRHLHTWIQ 180  
 QY 150 DNGGW 154  
 DB 181 DNGGW 185  
 RESULT 14  
 BCL2\_CHICK STANDARD; PRT; 233 AA.  
 ID BCL2\_CHICK  
 AC Q00709;  
 DT 01-APR-1993, integrated into UniProtKB/Swiss-Prot.  
 DT 01-APR-1993, sequence version 1.  
 DT 07-MAR-2006, entry version 45.  
 DE Apoptosis regulator Bcl-2.  
 GN Name=BCL2; Synonyms=BCL-2;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.  
 OK NCBI\_TaxID=9031;  
 RN (1)  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=92375724; PubMed=1508712;  
 RX Equchi Y., Ewert D.L., Teujimoto Y.;  
 RA "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=B-cell lymphoma;  
 RX MEDLINE=92379084; PubMed=1511008; DOI=10.1016/0167-4781(92)90064-7;  
 RA Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;  
 RT "Molecular cloning and DNA sequence analysis of cDNA encoding chicken  
 RT homologue of the Bcl-2 oncoprotein.";  
 RL Biochim. Biophys. Acta 1132:109-113(1992).  
 CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-X(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC motifs, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -!- TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen,  
 CC kidney, heart, ovary and brain, with the highest levels in the  
 CC thymus. In the embryo, highly levels expressed in all tissues with  
 CC high levels in the bursa of Fabricius.  
 CC -!- DOMAIN: The BH4 motif is required for anti-apoptotic activity and  
 CC for interaction with RAF-1 (By similarity).  
 CC -!- SIMILARITY: Belongs to the Bcl-2 family.  
 CC  
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 CC  
 CC -----  
 DR EMBL; D11382; BAA01978.1; -; Genomic\_DNA.  
 DR EMBL; Z11961; CAA78018.1; -; mRNA.  
 DR PIR; A37332; A37332.  
 DR PIR; S24390; S24390.  
 DR HSSP; P10415; 1G5M.  
 DR SMR; Q00709; 38-201  
 DR Ensembl; ENSGALG00000012885; Gallus gallus.  
 DR InterPro; IPR013278; Apop\_reg\_Bcl2.  
 DR InterPro; IPR012238; Bcl2\_apop\_reg.  
 DR InterPro; IPR000712; Bcl2\_BH.  
 DR InterPro; IPR003093; Bcl2\_BH4.  
 DR InterPro; IPR002475; Bcl2\_family.  
 DR InterPro; IPR004725; Bcl2\_reg.  
 DR Pfam; PF00452; Bcl-2; 1.  
 DR Pfam; PF02180; BH4; 1.  
 DR PIRSF; PIRSF001115; Bcl2 antiapop; 1.  
 DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
 DR PRINTS; PR01863; APOPRE5EC2.  
 DR PRINTS; PR01862; BCL2FAMILY.  
 DR SMART; SM00337; BCL; 1.  
 DR SMART; SM00265; BH4; 1.  
 DR TIGRFAMs; TIGR00865; bcl-2; 1.  
 DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE; PS01080; BH1; 1.  
 DR PROSITE; PS01258; BH2; 1.  
 DR PROSITE; PS01259; BH3; 1.  
 DR PROSITE; PS01260; BH4\_1; 1.  
 DR PROSITE; PS50063; BH4\_2; 1.  
 KW Apoptosis; Endoplasmic reticulum; Membrane; Mitochondrion;  
 KW Nuclear protein; Transmembrane.  
 FT CHAIN 1 233 Apoptosis regulator Bcl-2.

FT TRANSMEM 208 228 /FTid=PRO\_0000143051.  
 FT MOTIF 10 30 Potential\_  
 FT MOTIF 87 101 BH4.  
 FT MOTIF 130 149 BH1.  
 FT MOTIF 181 196 BH2.  
 FT CONFLICT 64 64 E -> S (in Ref. 2).  
 FT CONFLICT 67 82 GSAAASEVPPAELRP -> ARLLLVRCPLRGCA (in  
 FT Ref. 2).  
 FT CONFLICT 121 121 H -> T (in Ref. 2).  
 FT CONFLICT 139 139 G -> V (in Ref. 2).  
 SQ SEQUENCE 233 AA; 25687 MW; 52525555ACB6E4C3D CRC64;  
 Query Match 79.2%; Score 710.5; DB 1; Length 233;  
 Best Local Similarity 69.2%; Pred. No. 5.9e-59;  
 Matches 139; Conservative 7; Mismatches 20; Indels 35; Gaps 3;  
 QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRYEWDAGDD-----VEE 38  
 DB 1 MAHPGRGYDNREIVLKYIHYKLSQRYDWAAGEDRPVPAPAPAAAPAAAGASSH 60  
 QY 39 NRTEAP-EGTSEV-----VHLALROAGDDFSRRYRGDFPAEMSSQLHLTPFTA 85  
 DB 61 HRPEPPGSAASEVPPAELRPAPPGVHLALROAGDEFRRYORDFQAQMSQLHLTPFTA 120  
 QY 86 RGRFATVVEELFRDGVNMGRIVAFFRGGVCMVESVNNREMSPLVDNIALMTTEYLNRLHL 145  
 DB 121 HGRFVAVVEELFRDGVNMGRIVAFFRGGVCMVESVNNREMSPLVDNIALMTTEYLNRLHL 180  
 QY 146 TWIQDNGGWDFAVELYGPSMR 166  
 DB 181 NWIQDNGGWDFAVELYGNMSR 201  
 RESULT 15  
 Q6NTH7\_MOUSE  
 ID Q6NTH7\_MOUSE PRELIMINARY; PRT; 199 AA.  
 AC Q6NTH7;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 13.  
 DE B-cell leukemia/lymphoma 2.  
 GN Name=Bcl2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RX [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus gland;  
RA Strausberg R.;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
CC  
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CC  
CC EMBL; BC068988; AAH68988.1; -; mRNA.  
DR HSSP; P53563; IAF3.  
DR SMR; Q6NTH7; 41-192.  
DR Ensembl; ENSMUSG00000057329; Mus musculus.  
DR MGI; MGI:88138; Bcl2.  
DR GO; GO:0005829; C:cytosol; IDA.  
DR GO; GO:0005739; C:mitochondrion; IDA.  
DR GO; GO:0005515; F:protein binding; IPI.  
DR GO; GO:0006916; P:anti-apoptosis; IGI.  
DR GO; GO:0006916; P:anti-apoptosis; IDA.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR GO; GO:0001836; P:release of cytochrome c from mitochondria; IDA.  
DR InterPro; IPR013278; Apop reg Bcl2.  
DR InterPro; IPR012238; Bcl2\_apop\_reg.  
DR InterPro; IPR00712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF0452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR PIRSF; PIRSF001714; Bcl2\_apop\_reg; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; UNKNOWN\_1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PSS0063; BH4\_2; 1.  
SQ SEQUENCE 199 AA; 22281 MW; F13C8037262BA955 CRC64;

Query Match 77.4%; Score 694; DB 2; Length 199;  
Best Local Similarity 70.6%; Pred. No. 1.8e-57;  
Matches 139; Conservative 1; Mismatches 9; Indels 48; Gaps 3;  
  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDDVEENRTEAECT-----ES 49  
DB 1 MAQAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----ADAAPLCAATPGIFSFPES 55  
QY 50 E-----VHIALRQAGDDFSRRYRGDFAEMSSQ 77  
DB 56 NMPAVHRDMAARTSLRPLVATAGPALSPVPVHVHLLRRAGDDFSRRYRDFAEEMSSQ 115  
QY 78 LHLTPPTARGFATVVEELFRDGVNWRGRIVAFPEFGVNCVESVNRMSPLVDNIALWMT 137  
DB 116 LHLTPPTARGFATVVEELFRDGVNWRGRIVAFPEFGVNCVESVNRMSPLVDNIALWMT 175  
QY 138 EYLNRLHLTWIQDNGGW 154  
DB 176 EYLNRLHLTWIQDNGGW 192

Search completed: December 30, 2006, 12:12:39  
Job time : 303 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:07:51 ; Search time 39 Seconds  
(without alignments)  
409.538 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGTGYDNRREIVMKYIH.....WIQDNGWDFAVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.\*

2: p1r2.\*

3: p1r3.\*

4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	769.5	85.8	239	1 TVHUA1	transforming prote
2	760	84.7	236	2 I67432	BCL-2 - rat (fragm
3	759	84.6	236	2 I53744	gene bcl-2 protein
4	752	83.8	236	1 TVMSA1	transforming prote
5	752	83.8	236	2 JCT383	B-cell lymphoma 2
6	718.5	80.1	205	1 TVHUB1	transforming prote
7	710.5	79.2	233	2 A37332	transforming prote
8	689	76.8	199	1 TVMSB1	transforming prote
9	689	76.8	232	2 S24390	transforming prote
10	656.5	73.2	216	2 B37332	transforming prote
11	527	58.8	233	2 B47537	apoptosis regulato
12	511	57.0	233	2 I49056	BCL-X long - mouse
13	505	56.3	233	2 S51761	BCL-X protein - ra
14	484	55.1	214	2 I49057	bcl-x transmembran
15	489	54.5	227	2 JE0203	apoptosis regulato
16	489	54.5	233	2 I67431	BCL-X-long - rat
17	486	54.2	154	2 I58194	gene bcl-2 protein
18	415	46.3	190	2 A47537	apoptosis regulato
19	219	24.4	170	2 I49055	bcl-x short - mouse
20	213	23.7	176	2 I67435	gene bcl-xshort pr
21	175	19.5	211	2 S58873	Bak protein - huma
22	173	19.3	211	2 S58875	cdn-2 protein - hu
23	172.5	19.2	133	2 I53295	bcl-2-associated p
24	172	19.2	192	2 D47538	bcl-2-associated p
25	161	17.9	192	2 A47538	bcl-2-associated p
26	155.5	17.3	175	2 I39055	Bcl-2 related - hu
27	148.5	16.6	143	2 I39921	bcl-2-associated p
28	148	16.5	179	2 JCT255	Bax-delta protein
29	146.5	16.3	218	2 B47538	bcl-2-associated p

ALIGNMENTS

RESULT 1

TVHUA1

transforming protein bcl-2, splice form alpha - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1988 #sequence revision 07-Jun-1996 #text change 05-Oct-2004

C:Accession: C37332; A29409; S02452; A24428; A27622; B27622

R:Guchi, Y.; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari-

A:Reference number: A37332; MUID:92375724; PMID:1508712

A:Accession: C37332

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-239 <EGU>

A:Cross-references: UNIPROT:P10415; UNIPARC:UPI0000000D90E

A:Note: this report is a correction

R:Tsujimoto, Y.; Croce, C.M.

Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986

A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gen-

A:Reference number: A29409; MUID:86259760; PMID:3523487

A:Accession: A29409

A:Molecule type: mRNA

A:Residues: 1-95, 'A', '97-109, 'G', '111-236, 'S', '238-239 <TSU>

A:Cross-references: UNIPARC:UPI000002F8D7; GB:M13994; NID:G179366; PIDN:AAA51813.1; PID

A:Note: this sequence has been corrected in reference A37332

R:Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Koremcy

EMBO J. 7, 123-131, 1988

A:Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-

A:Reference number: S02452; MUID:88196071; PMID:2834197

A:Accession: S02452

A:Molecule type: mRNA

A:Residues: 1-239 <SET>

A:Cross-references: UNIPARC:UPI0000000D90E

R:Cleary, M.L.; Smith, S.D.; Sklar, J.

Cell 47, 19-28, 1986

A:Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunogl

A:Reference number: A24428; MUID:87002488; PMID:2875799

A:Accession: A24428

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-116, 'R', '118-239 <CLE>

A:Cross-references: UNIPARC:UPI0000035C80; GB:M14745; NID:G179370; PIDN:AAA35591.1; PID

R:Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J.; Bakshi, A.

Oncogene Res. 2, 263-275, 1988

A:Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma:

A:Reference number: A27622; MUID:88217344; PMID:3285301

A:Accession: A27622

A:Molecule type: mRNA

A:Residues: 1-58, 'T', '60-239 <HUA>

A:Cross-references: UNIPARC:UPI00000173303

A:Accession: B27622

A:Molecule type: DNA

A:Residues: 1-6, 'S', '8-58, 'T', '60-128, 'C', '130-239 <HUA2>

A;Cross-references: UNIPARC:UPI0000173303  
A;Note: the sequence was determined from the germline gene  
C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C;Genetics:  
A;Gene: GDB:BCL2  
A;Cross-references: GDB:119031; OMIM:151430  
A;Map position: 18q21.3-18q21.3  
C;Function:  
A;Description: blocks apoptosis in hematopoietic cells  
C;Superfamily: Bcl2 related apoptosis regulator  
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; proto

Query Match 85.8%; Score 769.5; DB 1; Length 239;  
Best Local Similarity 72.5%; Pred. No. 1.1e-66;  
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----DVEENRTEA 45  
Db 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGDVGAAAPGAPGIFSSQPGHTHPA 60  
Qy 46 GTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLOTPAAPGAAAGPALSPPVPVHLTLRQAGDDFSRRYRRDFAEMSSQLH 120  
Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180  
Qy 140 LNRHLHTWIQDNGWDADFVELYGFPSMR 166  
Db 181 LNRHLHTWIQDNGWDADFVELYGFPSMR 207

RESULT 2  
IG7432  
-BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: IG7432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equiva  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: 153295; MUID:95129487; PMID:7828536  
A;Accession: IG7432  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI00001707FF; EMBL:U34964; NID:G1004378; PI  
C;Superfamily: Bcl2 related apoptosis regulator

Query Match 84.7%; Score 760; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 8.8e-66;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----VVEENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQGYEWDTGDEDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPPVPVHLTLRRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180

RESULT 3  
IG7432  
-BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: IG7432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equiva  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: 153295; MUID:95129487; PMID:7828536  
A;Accession: IG7432  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI00001707FF; EMBL:U34964; NID:G1004378; PI  
C;Superfamily: Bcl2 related apoptosis regulator

Query Match 84.7%; Score 760; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 8.8e-66;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----VVEENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQGYEWDTGDEDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPPVPVHLTLRRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180

RESULT 3  
IG7432  
-BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Oct-2004  
C;Accession: IG7432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equiva  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: 153295; MUID:95129487; PMID:7828536  
A;Accession: IG7432  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI00001707FF; EMBL:U34964; NID:G1004378; PI  
C;Superfamily: Bcl2 related apoptosis regulator

Query Match 84.7%; Score 760; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 8.8e-66;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----VVEENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQGYEWDTGDEDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPPVPVHLTLRRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180

153744  
Gene bcl-2 protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Oct-2004  
C;Accession: I53744  
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.  
Gene 140, 291-292, 1994  
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.  
A;Reference number: 153744; MUID:94193015; PMID:8144041  
A;Accession: I53744  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: UNIPROT:P49950; UNIPARC:UPI000014728C; GB:L14680; NID:G408946; PIDN:  
C;Genetics:  
A;Gene: bcl-2  
C;Superfamily: Bcl2 related apoptosis regulator

Query Match 84.6%; Score 759; DB 2; Length 236;  
Best Local Similarity 73.0%; Pred. No. 1.1e-65;  
Matches 149; Conservative 3; Mismatches 14; Indels 38; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----VVEENRTEA 43  
Db 1 MAQAGRTGYDNREIVMKYIHVKLSQGYEWDTGDEDSAPLRAPTPGIFSFQPSNRTPA 60  
Qy 44 PEGTES-----EVHLALRQAGDDFSRRYRGDFAEMSSQLH 82  
Db 61 VHRDTAARTSPLRPLVANAGPALSPPVPVHLTLRRAGDDFSRRYRRDFAEMSSQLH 120  
Qy 83 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 142  
Db 121 FTARGRFATVVEELFRDGVNMGRIIVAFPEFGVCMCVSNREMSPLVDNIALWMTEY 180

RESULT 4  
TVM5A1  
transforming protein bcl-2-alpha - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004  
C;Accession: A25960; E37332  
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.  
Cell 49, 455-463, 1987  
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol  
A;Reference number: A90893; MUID:87187643; PMID:3032455  
A;Accession: A25960  
A;Molecule type: DNA  
A;Residues: 1-236 <NEG>  
A;Cross-references: UNIPARC:UPI00001470CA; GB:L31532; GB:M16506; NID:G468336; PIDN:AAA37  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: E37332  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A;Molecule type: DNA  
A;Residues: 1-33,'E',34-220,'AL',223-236 <EGU>  
A;Cross-references: UNIPARC:UPI0000173306  
C;Genetics:  
A;Gene: BCL2  
A;Introns: 192/3  
C;Superfamily: Bcl2 related apoptosis regulator  
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 83.8%; Score 752; DB 1; Length 236;  
Best Local Similarity 71.8%; Pred. No. 5.2e-65;  
Matches 150; Conservative 1; Mismatches 10; Indels 48; Gaps 3;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQGYEWDAAGD-----VVEENRTEA 43



Db 1 MAQAGRTGVDNREIVMKYIHYKLSQRYEWDAGD-----ADAAPLGAAPTGGIFSFPQES 55  
 QY 50 E-----VVHLALROAGDDFSRRYRGDFAEMSQ 77  
 Db 56 NMPAVHREMAARTSPRLVATAGPALSPVPCVHLTLRRAGDDFSRRYRDRDFAEMSQ 115  
 QY 78 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT 137  
 Db 116 LHLTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT 175  
 QY 138 EYLNRLHLTWIQDNGWDFAVELYGPSMR 166  
 Db 176 EYLNRLHLTWIQDNGWDFAVELYGPSMR 204

## RESULT 5

JC7383  
 B-cell lymphoma 2 protein - Chinese hamster  
 C:Species: Cricetulus griseus (Chinese hamster)  
 C:Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 05-Oct-2004  
 C:Accession: JC7383  
 R:Tomicic, M.T.; Christmann, M.; Kaina, B.  
 Biochem. Biophys. Res. Commun. 275, 899-903, 2000  
 A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.  
 A:Reference number: JC7383  
 A:Contents: Ovary  
 A:Accession: JC7383  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <TOM>  
 A:Cross-references: UNIPROT:Q9JJV8; UNIPARC:UPI0000126829; GB:AJ271720  
 C:Comment: This protein has anti-apoptotic function, and supports cell survival.  
 C:Genetics:  
 A:Gene: bcl-2  
 C:Superfamily: Bcl2 related apoptosis regulator  
 C:Keywords: B-cell lymphoma; ovary

Query Match 83.8%; Score 752; DB 2; Length 236;  
 Best Local Similarity 72.5%; Pred. No. 5.2e-65;  
 Matches 148; Conservative 2; Mismatches 16; Indels 38; Gaps 2;  
 QY 1 MAHAGRTGVDNREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEA 43  
 Db 1 MAQAGRTGVDNREIVMKYIHYKLSQRYEWDGVDAAPLGAAPTGGIFSFPQESNPTPA 60  
 QY 44 PE-----GTESEVHLALROAGDDFSRRYRGDFAEMSQLHLTP 82  
 Db 61 VHRDMAARTSPRLPIVATTGPTLSPPVPPVHLTLRRAGDDFSRRYRDRDFAEMSQLHLTP 120  
 QY 83 FTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT EYLN 142  
 Db 121 FTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT EYLN 180  
 QY 143 HLHTWTIQDNGWDFAVELYGPSMR 166  
 Db 181 HLHTWTIQDNGWDFAVELYGPSVR 204

## RESULT 6

TVHUB1  
 Transforming protein bcl-2, splice form beta - human  
 N:Alternate names: apoptosis regulator bcl-2  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 05-Oct-2004  
 C:Accession: B29409; I52566; D37332  
 R:Tsujiimoto, Y.; Croce, C.M.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986  
 A:Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene  
 A:Reference number: A29409; MUID:86259760; PMID:3523487  
 A:Accession: B29409  
 A:Molecule type: mRNA  
 A:Residues: 1-205 <TSU>  
 A:Cross-references: UNIPROT:P10415; UNIPARC:UPI0000043C0D; GB:M13995; NID:gl79368; PIDN:

R:Tanaka, S.; Louie, D.C.; Kant, J.A.; Reed, J.C.  
 Blood 79, 229-237, 1992  
 A:Title: Frequent incidence of somatic mutations in translocated BCL2 oncogenes of non-B  
 A:Reference number: I52566; MUID:92096610; PMID:1339299  
 A:Accession: I52566  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-131 <TAN>  
 A:Cross-references: UNIPARC:UPI000016B445; GB:S72602; NID:G241046; PIDN:AAD14111.1; PID  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: D37332  
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1-33, 'E', 34-95, 'T', 97-109, 'R', 111-205 <EGU>  
 A:Cross-references: UNIPARC:UPI0000173305  
 C:Genetics:  
 A:Gene: GDB:BCL2  
 A:Cross-references: GDB:119031; OMIM:151430  
 A:Map position: 18q21.3-18q21.3  
 C:Function:  
 A:Description: blocks apoptosis in hematopoietic cells  
 C:Superfamily: Bcl2 related apoptosis regulator  
 C:Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; prote

Query Match 80.1%; Score 718.5; DB 1; Length 205;  
 Best Local Similarity 71.8%; Pred. No. 7.4e-62;  
 Matches 140; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
 QY 1 MAHAGRTGVDNREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
 Db 1 MAHAGRTGVDNREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPFA 60  
 QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSQLH 79  
 Db 61 ASRDPVARTSPLOTPAAPGAAAGPALSPVPPVHLALROAGDDFSRRYRGDFAEMSQLH 120  
 QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT EY 139  
 Db 121 LTPFTARGFATVVEELFRDGVNMGRIVAFPEFGVCMVSVNREMSPLVDNIALMWT EY 180  
 QY 140 LNRHLHTWTIQDNGW 154  
 Db 181 LNRHLHTWTIQDNGW 195

## RESULT 7

A37332  
 Transforming protein (bcl-2-alpha) - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 05-Oct-2004  
 C:Accession: A37332; S35453  
 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
 Nucleic Acids Res. 20, 4187-4192, 1992  
 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a vari  
 A:Reference number: A37332; MUID:92375724; PMID:1508712  
 A:Accession: A37332  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-233 <EGU>  
 A:Cross-references: UNIPROT:Q00709; UNIPARC:UPI0000126828; EMBL:D11381  
 C:Genetics:  
 A:Introns: 189/3  
 C:Superfamily: Bcl2 related apoptosis regulator  
 C:Keywords: mitochondrion; transforming protein; transmembrane protein

Query Match 79.2%; Score 710.5; DB 2; Length 233;  
 Best Local Similarity 69.2%; Pred. No. 5.1e-61;  
 Matches 139; Conservative 7; Mismatches 20; Indels 35; Gaps 3;  
 QY 1 MAHAGRTGVDNREIVMKYIHYKLSQRYEWDAGD-----VBE 38

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Db 1 MAHGRGTYDNRREIVLVKIIHYKLSQRYGDMAGSDRPVPVPAPAPAPAAVAAGASSH 60
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLPFTA 85
Db 61 HRPEPPGSAASEVPPAEGRLPAPGCVHLALRQAGDFSRRYQRDFQMSQLHLPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLH 145
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLH 180
Qy 146 TWIQDNGWDADFVLYGSMR 166
Db 181 NWIQDNGWDADFVLYGSMR 201

RESULT 8
TWMS31
transforming protein bcl-2-beta - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C:Accession: B25960
R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homol
A:Reference number: A90893; MUID:87187643; PMID:3032455
A:Accession: B25960
A:Molecule type: DNA
A:Residues: 1-199 <NEG>
A:CROSS-references: UNIPROT:P10417; UNIPARC:UPI000002A4C2; GB:M16506; NID:g468335; PIDN:
C:Genetics:
A:Gene: BCL2
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: alternative splicing; transforming protein

Query Match 76.8%; Score 689; DB 1; Length 199;
Best Local Similarity 70.1%; Pred. No. 5e-59;
Matches 138; Conservative 1; Mismatches 10; Indels 48; Gaps 3;

Qy 1 MAHAGRTGYDNRREIVLVKIIHYKLSQRYGDMAGDDVFNRTAEPT-----ES 49
Db 1 MAAGRTGYDNRREIVLVKIIHYKLSQRYGDMAGD-----ADAAPLGAAPTGFISFPQES 55
Qy 50 E-----VHLALRQAGDDFSRRYRGDFAEMSSQ 77
Db 56 NPMPAVHREMAARTSPRLVATAGPALSPVPPCVHLTLRAGDDFSRRYRRDFAEMSSQ 115
Qy 78 LHLTPFTARGPATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWT 137
Db 116 LHLTPFTARGPATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWT 175
Qy 138 EYLNRLHWTIQDNGW 154
Db 176 EYLNRLHWTIQDNGW 192

RESULT 9
S24390
transforming protein (Bcl-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Oct-2004
C:Accession: S24390
R:Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.
Biochim. Biophys. Acta 1132, 109-113, 1992
A:Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue
A:Reference number: S24390; MUID:92379084; PMID:1511008
A:Accession: S24390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <CAZ>
A:CROSS-references: UNIPROT:Q00709; UNIPARC:UPI000017124D; EMBL:Z11961; NID:g62969; PIDN
C:Superfamily: Bcl2 related apoptosis regulator
C:Keywords: mitochondrion; transmembrane protein
```

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Query Match 76.8%; Score 689; DB 2; Length 232;
Best Local Similarity 66.3%; Pred. No. 6e-59;
Matches 136; Conservative 7; Mismatches 18; Indels 44; Gaps 3;

Qy 1 MAHAGRTGYDNRREIVLVKIIHYKLSQRYGDMAGDD-----VEE 38
Db 1 MAHPGRRGYDNRREIVLVKIIHYKLSQRYGDMAGDDRPVPVPAPAPAAVAAGASSH 60
Qy 39 NRTE-----APEGTESEVHVHLALRQAGDDFSRRYRGDFAEMSSQLHLT 81
Db 61 HRPSPPARLLVRCPLRGCAAPP-----VHLALRQAGDFSRRYQRDFQMSQLHLT 115
Qy 82 PPTARGPATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLN 141
Db 116 PPTATGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLN 175
Qy 142 RHLHTWIQDNGWDADFVLYGSMR 166
Db 176 RHLHTWIQDNGWDADFVLYGSMR 200

RESULT 10
B37332
transforming protein (bcl-2-beta) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 05-Oct-2004
C:Accession: B37332; S35452
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: B37332
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-216 <EGU>
A:CROSS-references: UNIPARC:UPI0000176495; EMBL:D11381; EMBL:D11382
C:Superfamily: Bcl2 related apoptosis regulator

Query Match 73.2%; Score 656.5; DB 2; Length 216;
Best Local Similarity 67.7%; Pred. No. 7.5e-56;
Matches 128; Conservative 7; Mismatches 19; Indels 35; Gaps 3;

Qy 1 MAHAGRTGYDNRREIVLVKIIHYKLSQRYGDMAGDD-----VEE 38
Db 1 MAHPGRRGYDNRREIVLVKIIHYKLSQRYGDMAGDDRPVPVPAPAPAAVAAGASSH 60
Qy 39 NRTEAP-EGTSEV-----VHLALRQAGDDFSRRYRGDFAEMSSQLHLPFTA 85
Db 61 HRPEPPGSAASEVPPAEGRLPAPGCVHLALRQAGDFSRRYQRDFQMSQLHLPFTA 120
Qy 86 RGRFATVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLH 145
Db 121 HGRFVAVVEELFRDGVNMGRIIVAFEFGGVCMCVSVNREMSPLVDNIALMWTYLNRLH 180
Qy 146 TWIQDNGW 154
Db 181 NWIQDNGW 189

RESULT 11
B47537
apoptosis regulator bcl-xL - human
A:Alternate names: bcl-2-related protein
N:Contains: apoptosis regulator bcl-xs
C:Species: Homo sapiens (man)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Oct-2004
A:Accession: B47537; C47537
R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;
Cell 74, 597-608, 1993
A:Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
A:Reference number: A47537; MUID:93364977; PMID:8358789
A:Accession: B47537
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A>Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-233 <BO1>  
A:Cross-references: UNIPROT:Q07817; UNIPARC:UPI000014624E; GB:L20121; NID:g510900; PIDN:  
F1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>  
A:Molecule type: mRNA  
A:Residues: 1-69, 'G', 71-125,189-233 <BO2>  
A:Cross-references: UNIPARC:UPI00002A4C4; GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:  
C:Genetics:  
A:Gene: GDB:BCL2L  
A:Cross-references: GDB:228079  
C:Superfamily: Bcl2 related apoptosis regulator  
C:Keywords: alternative splicing; apoptosis  
F1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>  
Query Match 58.8%; Score 527; DB 2; Length 233;  
Best Local Similarity 53.1%; Pred. No. 2.5e-43;  
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQRYGWDAGDDVEENRTEAPECTESEV----- 51  
DB 5 NRELVDVFLSYKLSQKGYMSQFSDVEENRTEAPECTESEMETPTPSAINGNPSWHLADSPA 64  
QY 52 -----VHLALRQAGDDPSRRYRGDFPFAEMSSQLHLTPPTARGRFA 90  
DB 65 VNGATGCHSSSLDAREVIPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVVNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNLDHLEPWIOE 184  
QY 151 NGGWDAFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 12  
I49056  
Query Match 57.0%; Score 511; DB 2; Length 233;  
Best Local Similarity 51.6%; Pred. No. 8.7e-42;  
Matches 99; Conservative 18; Mismatches 35; Indels 40; Gaps 1;  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49056  
R:Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49056  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-233 <RES>  
A:Cross-references: UNIPARC:UPI000002103C; EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PI  
C:Superfamily: Bcl2 related apoptosis regulator  
Query Match 57.0%; Score 511; DB 2; Length 233;  
Best Local Similarity 51.6%; Pred. No. 8.7e-42;  
Matches 99; Conservative 18; Mismatches 35; Indels 40; Gaps 1;  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49056  
R:Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49056  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-233 <RES>  
A:Cross-references: UNIPARC:UPI000002103C; EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PI  
C:Superfamily: Bcl2 related apoptosis regulator

65 VNGATGCHSSSLDAREVIPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVVNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNLDHLEPWIOE 184  
QY 151 NGGWDAFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 13  
I49057  
Query Match 56.3%; Score 505; DB 2; Length 233;  
Best Local Similarity 51.0%; Pred. No. 3.3e-41;  
Matches 98; Conservative 18; Mismatches 36; Indels 40; Gaps 1;  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Oct-2004  
C:Accession: S51761; S51762  
R:Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A:Reference number: S51761  
A:Accession: S51761  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-233 <MIC>  
A:Cross-references: UNIPROT:P53563; UNIPARC:UPI000017088C; EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PI  
A:Experimental source: embryonic; brain  
A:Accession: S51762  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-125,189-233 <M12>  
A:Cross-references: UNIPARC:UPI000017088D; EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PI  
A:Experimental source: embryonic; brain  
A:Note: smaller form due to splicing  
C:Genetics:  
A:Introns: 125/3  
C:Superfamily: Bcl2 related apoptosis regulator  
Query Match 56.3%; Score 505; DB 2; Length 233;  
Best Local Similarity 51.0%; Pred. No. 3.3e-41;  
Matches 98; Conservative 18; Mismatches 36; Indels 40; Gaps 1;  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49057  
R:Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49057  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-214 <RES>  
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DB 5 NQELVDVFLSYKLSQKGYMSQFSDVEENRTEAPECTESEPTPSAINGNPSWHLADSPA 64  
QY 51 -----VHLALRQAGDDPSRRYRGDFPFAEMSSQLHLTPPTARGRFA 90  
DB 65 VNGATGCHSSSLDAREVIPMAAVKQALREAGDFELRYRAFSDLTSQLHITPGTAYQSFE 124  
QY 91 TVVEELFRDGVNMGRIVAFPEFGVGVNREMSPLVDNIALWMTEYLNRLHHTWIOD 150  
DB 125 QVVNELFRDGVNMGRIVAFPEFGGALCVESVDKEMQVLSRIAAMWATYLNLDHLEPWIOE 184  
QY 151 NGGWDAFVELYG 162  
DB 185 NGGWDTFVDLYG 196  
RESULT 14  
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Query Match 56.3%; Score 505; DB 2; Length 233;  
Best Local Similarity 51.0%; Pred. No. 3.3e-41;  
Matches 98; Conservative 18; Mismatches 36; Indels 40; Gaps 1;  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Oct-2004  
C:Accession: I49057  
R:Pang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A:Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A:Reference number: I49055; MUID:95052604; PMID:7963517  
A:Accession: I49057  
A:Molecule type: mRNA  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Residues: 1-214 <RES>



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: December 30, 2006, 12:26:47 ; Search time 44 Seconds  
(without alignments)  
369.134 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRREIVNMYKH.....WIQDNGWDFAVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390055 seqs, 97842647 residues

Total number of hits satisfying chosen parameters: 390055

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA\_New.\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771.5	86.0	239	7 US-11-187-863-4	Sequence 4, Appli
2	763.5	85.1	239	6 US-10-549-711-8	Sequence 8, Appli
3	763.5	85.1	239	7 US-11-009-357-8	Sequence 8, Appli
4	757.5	84.4	239	7 US-11-021-541-1705	Sequence 1705, Ap
5	757.5	84.4	236	7 US-11-021-541-1707	Sequence 1707, Ap
6	718.5	80.1	205	6 US-10-549-711-10	Sequence 10, Appl
7	528	58.9	247	6 US-10-540-898-743	Sequence 743, App
8	527	58.8	233	6 US-10-533-519-1168	Sequence 1168, Ap
9	527	58.8	233	6 US-10-533-519-1688	Sequence 1688, Ap
10	527	58.8	233	7 US-11-009-357-7	Sequence 2, Appli
11	527	58.8	233	7 US-11-296-725-2	Sequence 2, Appli
12	527	58.8	233	7 US-11-371-354-59735	Sequence 59735, A
13	527	58.8	233	7 US-11-021-541-1709	Sequence 1709, Ap
14	512	57.1	340	6 US-10-540-898-740	Sequence 740, App
15	377.5	42.1	193	7 US-11-301-951-2	Sequence 2, Appli
16	376.5	42.0	193	7 US-11-301-951-4	Sequence 4, Appli
17	368.5	41.9	193	7 US-11-301-951-6	Sequence 6, Appli
18	375.5	41.1	193	7 US-11-301-951-8	Sequence 8, Appli
19	232	25.9	170	7 US-11-021-541-1721	Sequence 1721, Ap
20	175	19.5	211	7 US-11-371-354-72633	Sequence 72633, A
21	175	19.5	211	7 US-11-021-541-1715	Sequence 1715, Ap
22	174	19.4	192	7 US-11-021-541-1719	Sequence 1719, Ap
23	174	19.4	192	7 US-11-158-863-2	Sequence 2, Appli
24	171.5	19.1	211	6 US-10-538-002-95	Sequence 95, Appl
25	161	17.9	191	7 US-11-415-342-46	Sequence 46, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-187-863-4

; Sequence 4, Application US/11187863

; Publication No. US20060110793A1

; GENERAL INFORMATION:

; APPLICANT: GOLDENBERG, DAVID M.

; APPLICANT: QU, ZHENGXING

; APPLICANT: HORAK, EVA

; APPLICANT: HORAK, IVAN D.

; APPLICANT: CHANG, CHIEN HSING

; APPLICANT: ROSSI, EDMOND A.

; APPLICANT: YANG, JENG-DAR

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INCREASING LONGEVITY AND

; TITLE OF INVENTION: PROTEIN YIELD FROM A CELL CULTURE

; FILE REFERENCE: 40923-0194US1

; CURRENT APPLICATION NUMBER: US/11/187,863

; CURRENT FILING DATE: 2005-07-25

; PRIOR APPLICATION NUMBER: 60/590,349

; PRIOR FILING DATE: 2004-07-23

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 3.3

; SEQ ID NO 4

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: protein

; US-11-187-863-4

Query Match

Best Local Similarity 86.0%; Score 771.5; DB 7; Length 239;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY	1	MAHAGRTGYDNRREIVNMYKHYSQRGYEWDA	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79
DB	1	MAHAGRTGYDNRREIVNMYKHYSQRGYEWDA	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 120
QY	35	-----DVEENRTEAPECTES-----	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 139
DB	61	ASRDVPVAREEPLQTPAAPGAAAGPALEPVPV	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 180
QY	80	LTPTTARGFAATVVEELFRDGVNNGRIIVAF	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 180
DB	121	LTPTTARGFAATVVEELFRDGVNNGRIIVAF	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 180
QY	140	LNRLHLTWTIQDNGWDADFVELYGPSMR	-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 166

Sequence 2, Appli  
Sequence 58719, A  
Sequence 1717, Ap  
Sequence 3000, Ap  
Sequence 1071, Ap  
Sequence 55127, A  
Sequence 123, App  
Sequence 6, Appli  
Sequence 27, Appli  
Sequence 4, Appli  
Sequence 18, Appli  
Sequence 5817, Ap  
Sequence 210, App  
Sequence 6583, Ap  
Sequence 9928, Ap  
Sequence 9927, Ap  
Sequence 9926, Ap  
Sequence 65929, A  
Sequence 1864, Ap

26 161 17.9 192 6 US-10-550-280-2  
27 161 17.9 192 7 US-11-371-354-58719  
28 161 17.9 192 7 US-11-021-541-1717  
29 155.5 17.3 175 6 US-10-511-937-3000  
30 155.5 17.3 175 6 US-10-533-519-1071  
31 155.5 17.3 175 7 US-11-371-354-55127  
32 146.5 16.3 350 6 US-10-533-519-123  
33 102.5 11.4 328 6 US-10-550-280-6  
34 102.5 11.4 332 6 US-10-550-280-4  
35 88 9.8 18 7 US-11-409-944-27  
36 85 9.5 831 7 US-11-265-532A-4  
37 84 9.4 14 7 US-11-259-640A-18  
38 82 9.1 811 6 US-10-805-394-5817  
39 81 9.0 995 7 US-11-357-421-210  
40 80.5 9.0 495 6 US-10-805-394-6583  
41 77.5 8.6 864 6 US-10-953-349-9928  
42 77.5 8.6 866 6 US-10-953-349-9927  
43 77.5 8.6 951 6 US-10-953-349-9926  
44 77 8.6 223 7 US-11-371-354-65929  
45 76.5 8.5 320 6 US-10-526-324-1864

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Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 2
US-10-549-711-8
; Sequence 8, Application US/10549711
; Publication No. US20060223768A1
; GENERAL INFORMATION:
; APPLICANT: Milner, Josephine
; TITLE OF INVENTION: Regulation of Gene Expression
; FILE REFERENCE: 4100-0001
; CURRENT APPLICATION NUMBER: US/10/549,711
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: GB 0306148.8
; PRIOR FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-549-711-8

Query Match      85.1%; Score 763.5; DB 6; Length 239;
Best Local Similarity 72.5%; Pred. No. 3e-73;
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGD----- 34
Db      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGDVGAAAPGAAPAGPAGFFSQPGHTPTA 60

Qy      35 -----DVEENRTEAPGTE-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLTLRQAGDDFSRRYRRDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 3
US-11-009-357-8
; Sequence 8, Application US/11009357
; Publication No. US20060127376A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Ute
; TITLE OF INVENTION: Methods and Compositions for Modulating Apoptotic Pathways
; FILE REFERENCE: STONYB-09615
; CURRENT APPLICATION NUMBER: US/11/009,357
; CURRENT FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-357-8

Query Match      85.1%; Score 763.5; DB 7; Length 239;
Best Local Similarity 72.5%; Pred. No. 3e-73;
Matches 150; Conservative 2; Mismatches 14; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGD----- 34
Db      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGDVGAAAPGAAPAGPAGFFSQPGHTPTA 60

Qy      35 -----DVEENRTEAPGTE-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLTLRQAGDDFSRRYRRDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 4
US-11-021-541-1705
; Sequence 1705, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DMR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1705
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-541-1705

Query Match      84.4%; Score 757.5; DB 7; Length 239;
Best Local Similarity 71.5%; Pred. No. 1.3e-72;
Matches 148; Conservative 3; Mismatches 15; Indels 41; Gaps 2;

Qy      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGD-----DVEENRTEAPE 45
Db      1 MAHAGRTGYDNRREIVMKYIHYKLSQGYEWDAAGDVGAAAPGAAPAGPAGFFSQPGHTPTA 60

Qy      46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db      61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPPVHLLTLRQAGDDFSRRYRRDFAEMSSQLH 120

Qy      80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 139
Db      121 LTPFTARGCFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNRMSPLVDNIALWMTEY 180

Qy      140 LNRHLHTWIQDNGWDADFVLYGFSMR 166
Db      181 LNRHLHTWIQDNGWDADFVLYGFSMR 207

RESULT 5
US-11-021-541-1707
; Sequence 1707, Application US/11021541
; Publication No. US20060287259A1
; GENERAL INFORMATION:
; APPLICANT: REICH, SAMUEL JOTHAM
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COMBINED THERAPY OF DISEASE
; FILE REFERENCE: DMR-04-1324R
; CURRENT APPLICATION NUMBER: US/11/021,541
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,099
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 1733
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1707
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-021-541-1707
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Query Match 84.4%; Score 757; DB 7; Length 236;  
Best Local Similarity 72.2%; Pred. No. 1.5e-72;  
Matches 151; Conservative 1; Mismatches 9; Indels 48; Gaps 3;  
QY 1 MAHAGTGYDNRREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAPECT-----BS 49  
DB 1 MAQAGRTGYDNRREIVMKYIHYKLSQRGYEWDAAGD-----ADAAPLGAAPTGGIFSPQPS 55  
QY 50 E-----VHLALRQAGDDPSRRYRGDFAEMSSQ 77  
DB 56 NMPAVHRDMAARTSLRPLVATAGPALSPVPVHLTLRRAGDDPSRRYRGDFAEMSSQ 115  
QY 78 LHLTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 137  
DB 116 LHLTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWT 175  
QY 138 EYLNRLHWTIODNGWDFAVELYGPMSR 166  
DB 176 EYLNRLHWTIODNGWDFAVELYGPMSR 204  
RESULT 6  
US-10-549-711-10  
; Sequence 10, Application US/10549711  
; Publication No. US20060223768A1  
; GENERAL INFORMATION:  
; APPLICANT: Milner, Josephine  
; TITLE OF INVENTION: Regulation of Gene Expression  
; FILE REFERENCE: 4100-0001  
; CURRENT APPLICATION NUMBER: US/10/549,711  
; CURRENT FILING DATE: 2005-09-16  
; PRIOR APPLICATION NUMBER: GB 0306148.8  
; PRIOR FILING DATE: 2003-03-18  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-549-711-10

Query Match 80.1%; Score 718.5; DB 6; Length 205;  
Best Local Similarity 71.8%; Pred. No. 1.5e-68;  
Matches 140; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGTGYDNRREIVMKYIHYKLSQRGYEWDAAGD-----DVEENRTAPE 45  
DB 1 MAHAGTGYDNRREIVMKYIHYKLSQRGYEWDAAGDVGAAAPGAPGIFSPQGHPPHA 60  
QY 46 GTES-----EVHLALRQAGDDPSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLOTTPAAGAAAGPALSPVPVHLALRQAGDDPSRRYRGDFAEMSSQLH 120  
QY 80 LTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTY 139  
DB 121 LTPPTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTY 180  
QY 140 LNRHLHWTIODNGGW 154  
DB 181 LNRHLHWTIODNGGW 195  
RESULT 7  
US-10-540-898-743  
; Sequence 743, Application US/10540898  
; Publication No. US20060166213A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: CHIR0056-101 (PPO23367.0003)  
; CURRENT APPLICATION NUMBER: US/10/540,898  
; CURRENT FILING DATE: 2005-06-27

; PRIOR APPLICATION NUMBER: US 10/330,773  
; PRIOR FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 743  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-540-898-743  
Query Match 58.9%; Score 528; DB 6; Length 247;  
Best Local Similarity 53.7%; Pred. No. 3.4e-48;  
Matches 102; Conservative 17; Mismatches 33; Indels 38; Gaps 1;  
QY 11 NREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAPECTSEV----- 51  
DB 21 NRELVDVFLSYKLSQKGYSWQSOFSDVEENRTAPECTSEMPSSAINGNPSWHLADSPAVN 80  
QY 52 -----VHLALRQAGDDPSRRYRGDFAEMSSQLHLPFTTARGRFA 92  
DB 81 GATGHSSSLDAREVPMMAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSF 140  
QY 93 VEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTYLNRLHWTIODNG 152  
DB 141 VNELFRDGVNMGRIIVAFEFEGGALCVESVDKEMQVLVSRIAAAMATYLNLDHLEPWIQENG 200  
QY 153 GMDAFVELYG 162  
DB 201 GMDTFVELYG 210  
RESULT 8  
US-10-533-519-1168  
; Sequence 1168, Application US/10533519  
; Publication No. US20060263774A1  
; GENERAL INFORMATION:  
; APPLICANT: CLARK, HILARY  
; APPLICANT: SCHOENFELD, JILL  
; APPLICANT: VANLOOKEREN, MENNO  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WOOD, WILLIAM I.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE  
; TITLE OF INVENTION: RELATED DISEASES  
; FILE REFERENCE: P1984R1 US  
; CURRENT APPLICATION NUMBER: US/10/533,519  
; CURRENT FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: PCT/US03/34312  
; PRIOR FILING DATE: 2003-10-30  
; PRIOR APPLICATION NUMBER: US 60/423,394  
; PRIOR FILING DATE: 2002-11-01  
; NUMBER OF SEQ ID NOS: 2517  
; SEQ ID NO 1168  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-533-519-1168  
Query Match 58.8%; Score 527; DB 6; Length 233;  
Best Local Similarity 53.1%; Pred. No. 4e-48;  
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;  
QY 11 NREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAPECTSEV----- 51  
DB 5 NRELVDVFLSYKLSQKGYSWQSOFSDVEENRTAPECTSEMPSSAINGNPSWHLADSPA 64  
QY 52 -----VHLALRQAGDDPSRRYRGDFAEMSSQLHLPFTTARGRFA 90  
DB 65 VNGATGHSSSLDAREVPMMAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSF 124  
QY 91 TVVEELFRDGVNMGRIIVAFEFEGGVMCVSVNREMSPLVDNIALMWTYLNRLHWTIOD 150  
DB 125 QVNNELFRDGVNMGRIIVAFEFEGGALCVESVDKEMQVLVSRIAAAMATYLNLDHLEPWIOE 184

```
Qy 151 NGGWDFAVELYG 162
Db 185 NGGWDTFVELYG 196

RESULT 9
US-10-533-519-1688
; Sequence 1688, Application US/10533519
; Publication No. US20060263774A1
; GENERAL INFORMATION:
; APPLICANT: CLARK, HILARY
; APPLICANT: SCHOENFELD, JILL
; APPLICANT: VANLOOKEREN, MENNO
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF THE TREATMENT OF IMMUNE
; FILE REFERENCE: P1984R1 US
; CURRENT APPLICATION NUMBER: US/10/533,519
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: PCT/US03/34312
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,394
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 2517
; SEQ ID NO 1688
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-533-519-1688

Query Match 58.8%; Score 527; DB 6; Length 233;
Best Local Similarity 53.1%; Pred. No. 4e-48;
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;

Qy 11 NREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAEPEGTSEV----- 51
Db 5 NRELVDVFLSYKLSQKGYSWQFSDVEENRTAEPEGTSEMETPSAINGNPSWHLADSPA 64
Qy 52 -----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFA 90
Db 65 VNGATGHSSSLDAREVIPAAMVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYOSFE 124
Qy 91 TVVEELFRDGVNMGRIVAFFFGVCMVESVNRREMSPLVDNIALWMTEYLNRLHLHTWIQD 150
Db 125 QVNVNELFRDGVNMGRIVAFFFGGALCVESVDKEMQVLVSRIAAMWATYLNLDHLEPWIOE 184
Qy 151 NGGWDFAVELYG 162
Db 185 NGGWDTFVELYG 196

RESULT 10
US-11-009-357-7
; Sequence 7, Application US/11009357
; Publication No. US20060127376A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Ute
; TITLE OF INVENTION: Methods and Compositions for Modulating Apoptotic Pathways
; FILE REFERENCE: STONYB-09615
; CURRENT APPLICATION NUMBER: US/11/009,357
; CURRENT FILING DATE: 2004-12-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-357-7

Query Match 58.8%; Score 527; DB 7; Length 233;
Best Local Similarity 53.1%; Pred. No. 4e-48;
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;

Qy 11 NREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAEPEGTSEV----- 51
Db 5 NRELVDVFLSYKLSQKGYSWQFSDVEENRTAEPEGTSEMETPSAINGNPSWHLADSPA 64
Qy 52 -----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFA 90
Db 65 VNGATGHSSSLDAREVIPAAMVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYOSFE 124
Qy 91 TVVEELFRDGVNMGRIVAFFFGVCMVESVNRREMSPLVDNIALWMTEYLNRLHLHTWIQD 150
Db 125 QVNVNELFRDGVNMGRIVAFFFGGALCVESVDKEMQVLVSRIAAMWATYLNLDHLEPWIOE 184
Qy 151 NGGWDFAVELYG 162
Db 185 NGGWDTFVELYG 196

RESULT 11
US-11-296-725-2
; Sequence 2, Application US/11296725
; Publication No. US20060199780A1
; GENERAL INFORMATION:
; APPLICANT: Naval Medical Research Center
; APPLICANT: Thompson, Craig B.
; TITLE OF INVENTION: Methods for modulating T cell survival by modulating BCL-XL
; FILE REFERENCE: 11/296,725
; CURRENT APPLICATION NUMBER: US/11/296,725
; CURRENT FILING DATE: 2005-12-02
; PRIOR APPLICATION NUMBER: 09/707,087
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: human
US-11-296-725-2

Query Match 58.8%; Score 527; DB 7; Length 233;
Best Local Similarity 53.1%; Pred. No. 4e-48;
Matches 102; Conservative 17; Mismatches 33; Indels 40; Gaps 1;

Qy 11 NREIVMKYIHYKLSQRGYEWDAAGDDVEENRTAEPEGTSEV----- 51
Db 5 NRELVDVFLSYKLSQKGYSWQFSDVEENRTAEPEGTSEMETPSAINGNPSWHLADSPA 64
Qy 52 -----VHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFA 90
Db 65 VNGATGHSSSLDAREVIPAAMVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYOSFE 124
Qy 91 TVVEELFRDGVNMGRIVAFFFGVCMVESVNRREMSPLVDNIALWMTEYLNRLHLHTWIQD 150
Db 125 QVNVNELFRDGVNMGRIVAFFFGGALCVESVDKEMQVLVSRIAAMWATYLNLDHLEPWIOE 184
Qy 151 NGGWDFAVELYG 162
Db 185 NGGWDTFVELYG 196

RESULT 12
US-11-371-354-59735
; Sequence 59735, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; IDENTIFYING MATCHED REAGENTS
```



Qy	52	-----VHLALRQAGDDFSRRYRGDFABMSQLHLTPPTARGRA 90
Db	65	VNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSQLHITPGTAQSPF 124
Qy	91	TVVEELFRDGVNMGRIVAFEFGGVMCVSVNREMSPLVDNIALMWTYLNRLHHTWIQD 150
Db	125	QVNVNELFRDGVNMGRIVAFEFGGALCVESVDKEMQVLVSRIAAMWATYLNHLEPWIOE 184
Qy	151	NGGWDFAFVELYG 162
Db	185	NGGWDTFVELYG 196
RESULT 14		
US-10-540-898-740		
; Sequence 740, Application US/10540898		
; Publication No. US20060166213A1		
; GENERAL INFORMATION:		
; APPLICANT: David W. Morris		
; APPLICANT: Marc Malandro		
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer		
; FILE REFERENCE: CHIR0056-101 (PP023367.0003)		
; CURRENT APPLICATION NUMBER: US/10/540,898		
; CURRENT FILING DATE: 2005-06-27		
; PRIOR APPLICATION NUMBER: US 10/330,773		
; PRIOR FILING DATE: 2002-12-27		
; NUMBER OF SEQ ID NOS: 981		
; SOFTWARE: FastSeq for Windows Version 4.0		
; SEQ ID NO 740		
; LENGTH: 340		
; TYPE: PRT		
; ORGANISM: Mus musculus		
US-10-540-898-740		
Query Match 57.1%; Score 512; DB 6; Length 340;		
Best Local Similarity 50.8%; Pred. No. 2.6e-46;		
Matches 100; Conservative 18; Mismatches 39; Indels 40; Gaps 1		
Qy	6	RTGYDNREIVKVIHYKLSQRGYEWDAAGDDVEENRTEAPEGTESE-----50
Db	92	RADFSNRELVDVFLSYKLSQKGYWSQFSVDVEENRTEAPEETAEARETSAINGNPSWHL 151
Qy	51	-----VVHLALRQAGDDFSRRYRGDFRRAESQLHLTPFTA 85
Db	152	ADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSQLHITPGTA 211
Qy	86	RGRFATVVEELFRDGVNMGRIVAFEFGGVMCVSVNREMSPLVDNIALMWTYLNRLH 145
Db	212	YQSFEQVNVNELFRDGVNMGRIVAFEFGGALCVESVDKEMQVLVSRIAAMWATYLNHLE 271
Qy	146	TWQDNGGWDFAFVELYG 162
Db	272	PWQENGWDTFVDLYG 288
RESULT 15		
US-11-301-951-2		
; Sequence 2, Application US/11301951		
; Publication No. US2006090214A1		
; GENERAL INFORMATION:		
; APPLICANT: Cory, Suzanne		
; APPLICANT: Adams, Jerry		
; APPLICANT: Print, Cris		
; APPLICANT: Gibson, Leonie		
; APPLICANT: Koentgen, Frank		
; TITLE OF INVENTION: A METHOD OF TREATMENT AND AN ANIMAL MODEL USEFUL FOR		
; TITLE OF INVENTION: SAME		
; FILE REFERENCE: 13464		
; CURRENT APPLICATION NUMBER: US/11/301,951		
; CURRENT FILING DATE: 2005-12-13		
; PRIOR APPLICATION NUMBER: US/09/508,745		



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OM protein - protein search, using sw model

Run on: December 30, 2006, 12:24:51 ; Search time 181 Seconds  
(without alignments)  
424.827 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRREIVMKYIH.....WIQDNGGWDFAVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	796	88.7	200	5	US-10-981-873-45
2	781.5	87.1	239	2	US-08-726-211-5
3	781.5	87.1	239	3	US-09-993-420A-8
4	781.5	87.1	239	4	US-10-141-618-12
5	781.5	87.1	239	4	US-10-053-645A-21
6	781.5	87.1	239	4	US-10-387-961A-5
7	781.5	87.1	239	4	US-10-003-632C-1
8	781.5	87.1	239	4	US-10-003-632C-3
9	781.5	87.1	239	4	US-10-148-953A-1
10	781.5	87.1	239	5	US-10-825-282-46
11	781.5	87.1	239	5	US-10-961-458-21
12	778.5	86.8	239	4	US-10-148-953A-2
13	778.5	86.8	239	4	US-10-148-953A-4
14	778.5	86.8	239	4	US-10-297-321-2
15	777.5	86.7	239	4	US-10-148-953A-5
16	775.5	86.5	239	4	US-10-148-953A-3
17	769.5	85.8	239	4	US-10-277-693A-10
18	769.5	85.8	239	4	US-10-003-632C-10
19	769.5	85.8	239	4	US-10-003-632C-13
20	769.5	85.8	239	6	US-11-037-713-5
21	763.5	85.1	239	4	US-10-101-482-12
22	763.5	85.1	239	4	US-10-072-830-2
23	763.5	85.1	239	4	US-10-450-366-4
24	763.5	85.1	239	4	US-10-770-668-16
25	763.5	85.1	239	5	US-10-887-066-2
26	763.5	85.1	239	6	US-11-082-485-12
27	757	84.4	236	4	US-10-087-192-1953

28	753.5	84.0	239	4	US-10-659-705-4	Sequence 4, Appli
29	752	83.8	236	4	US-10-277-693A-11	Sequence 11, Appl
30	718.5	80.1	205	2	US-08-726-211-7	Sequence 7, Appli
31	718.5	80.1	205	3	US-09-952-278-4	Sequence 4, Appli
32	718.5	80.1	205	4	US-10-053-645A-23	Sequence 23, Appli
33	718.5	80.1	205	4	US-10-387-961A-7	Sequence 7, Appli
34	718.5	80.1	205	4	US-10-003-632C-2	Sequence 2, Appli
35	718.5	80.1	205	4	US-10-003-632C-11	Sequence 11, Appli
36	718.5	80.1	205	5	US-10-961-458-23	Sequence 23, Appli
37	706.5	78.8	205	4	US-10-087-192-1956	Sequence 1956, Ap
38	704.5	78.5	155	4	US-10-158-769-1	Sequence 1, Appli
39	704.5	78.5	155	4	US-10-729-156-1	Sequence 1, Appli
40	701.5	78.2	233	4	US-10-659-705-3	Sequence 3, Appli
41	608	67.8	154	4	US-10-007-573-3	Sequence 40224, A
42	584	65.1	231	5	US-10-450-763-40224	Sequence 2, Appli
43	556	62.0	152	4	US-10-158-769-2	Sequence 2, Appli
44	556	62.0	152	4	US-10-729-156-2	Sequence 8, Appli
45	546	60.9	199	4	US-10-402-017-8	

#### ALIGNMENTS

#### RESULT 1

US-10-981-873-45  
; Sequence 45, Application US/10981873  
; Publication No. US20050250680A1  
; GENERAL INFORMATION:  
; APPLICANT: Malensky, Loren D.  
; APPLICANT: Korameyer, Stanley J.  
; APPLICANT: Verdine, Gregory  
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 00530-124001  
; CURRENT APPLICATION NUMBER: US/10/981,873  
; PRIOR FILING DATE: 2004-11-05  
; PRIOR APPLICATION NUMBER: US 60/517,848  
; PRIOR FILING DATE: 2003-11-05  
; PRIOR APPLICATION NUMBER: US 60/591,548  
; PRIOR FILING DATE: 2004-07-27  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 200  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-981-873-45

Query Match 88.7%; Score 796; DB 5; Length 200;  
Best Local Similarity 90.5%; Pred. No. 1.3e-80;  
Matches 152; Conservative 0; Mismatches 14; Indels 2; Gaps 1;  
  
QY 1 MAHAGRTGYDNRREIVMKYIHKLSQSGYEWADGDDVEENRTEAPEGTE--SEVVHIALRQ 58  
Db 1 MAHAGRTGYDNRREIVMKYIHKLSQSGYEWADGDDVEENRTEAPEGTE--SEVVHIALRQ 60  
  
QY 59 AGDDFSRRYRGDFAEWSSQLHLPETARGRFATVVEELFRDGVNMGRIVAFVFEFGGVMCV 118  
Db 61 AGDDFSRRYRGDFAEWSSQLHLPETARGRFATVVEELFRDGVNMGRIVAFVFEFGGVMCV 120  
  
QY 119 ESNVREMSPLVDNIALWMTEYLNRLHHTWIQDNGGWDFAVELYGPSMR 166  
Db 121 ESNVREMSPLVDNIALWMTEYLNRLHHTWIQDNGGWDFAVELYGPSMR 168

#### RESULT 2

US-08-726-211-5  
; Sequence 5, Application US/08726211  
; Publication No. US20030012812A1  
; GENERAL INFORMATION:  
; APPLICANT: Tormo, Mar  
; APPLICANT: Tari, Ana M.  
; APPLICANT: Lopez-Berestein, Gabriel

TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
 TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P.O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: United States of America  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/726,211  
 FILING DATE: Concurrently Herewith  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Wilson, Mark B.  
 REGISTRATION NUMBER: 37,259  
 REFERENCE/DOCKET NUMBER: UTXC:504  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (512) 474-7577  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 239 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PS-08-726-211-5

Query Match	87.1%	Score	781.5	DB 2	Length	239			
Best Local Similarity	73.4%	Pred. No.	7.2e-79						
Matches	152	Conservative	2	Mismatches	12	Indels	41	Gaps	2
Qy	1	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDA	GDG	-----DVEENRTEAPE	45				
Db	1	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDA	GDVGAAPCAAPAGIFSSQPGHTHPA	60					
Qy	46	GTES	-----EVHIALRQAGDDPSRRYRGDFAEMSSQLH	79					
Db	61	ASRDPVARTSPLQTAPAAPGAAAGPALSPVPV	PVHIALRQAGDDPSRRYRGDFAEMSSQLH	120					
Qy	80	LTPPTAGRGATVVEELFRDGVNNGRIVAFPEFG	GVWCVESVNREMSPLVDNIALWMTYE	139					
Db	121	LTPPTAGRGATVVEELFRDGVNNGRIVAFPEFG	GVWCVESVNREMSPLVDNIALWMTYE	180					
Qy	140	LNRLHWTWIDNGGWDAPVELYGPSMR	166						
Db	181	LNRLHWTWIDNGGWDAPVELYGPSMR	207						

RESULT 3  
US-09-993-420A-8  
; Sequence 8, Application US/09993420A  
; Publication No. US20030064476A1  
; GENERAL INFORMATION:  
; APPLICANT: Horvitz, H. Robert  
; APPLICANT: Hengartner, Michael  
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A  
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 01997/201006  
; CURRENT APPLICATION NUMBER: US/09/993,420A  
; CURRENT FILING DATE: 5001-11-09  
; PRIOR APPLICATION NUMBER: 09/234,186  
; PRIOR FILING DATE: 1999-01-20  
; PRIOR APPLICATION NUMBER: 07/898,933  
; PRIOR FILING DATE: 1992-06-12  
; PRIOR APPLICATION NUMBER: 07/927,681

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; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 239
; TYPE: prt
; ORGANISM: Homo sapiens
; US-09-993-420A-8

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Query Match	87.1%	Score	781.5	DB	3	Length	239
Best Local Similarity	73.4%	Pred. No.	7.2e-79				
Matches	152	Conservative	2	Mismatches	12	Indels	41
Gaps							
QY	1	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDA	DAGD	-----DVEENR	TAPE	45	
Db	1	MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDA	DGVGAAPGAA	PAAPG	CFSSQPGHT	HPHA	60
QY	46	GTES	-----EVH	LALRQAGDD	FSRRYRGD	FAEMSSQLH	79
Db	61	ASRDPVARTSPLQTPAAPAGAAAGPALS	PVPVPV	VHLLALRQAGDD	FSRRYRGD	FAEMSSQLH	120
QY	80	LTPPTAGRGATVVEELFRQGVN	GRIVAF	FFFGV	CMVCESVN	REMSPLVD	NIALWMTEY
Db	121	LTPPTAGRGATVVEELFRQGVN	GRIVAF	FFFGV	CMVCESVN	REMSPLVD	NIALWMTEY
QY	140	LNRLHWTWIQDGGWDAFVELY	GPSMR	166			
Db	181	LNRLHWTWIQDGGWDAFVELY	GPSMR	207			

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RESULT 4
US-10-141-618-12
; Sequence 12, Application US/10141618
; Publication No. US20030165887A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Methods For Determining the Prognosis
; OF INVENTION: For Cancer Patients Using Tucan
; FILE REFERENCE: P-LJ 5254
; CURRENT APPLICATION NUMBER: US/10/141.618
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,233
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/356,934
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US 09/388,221
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-141-618-12

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Query Match	87.1%	Score 781.5	DB 4	Length 239
Best Local Similarity	73.4%	Pred. No. 7.2e-79		
Matches 152	Conservative 2	Mismatches 12	Indels 41	Gaps 2

  

Qy	1	MAHAGRTGYDNRREIMVKYIHKLSQGVENDAGD-----DVEENRTTAE	45
Db	1	MAHAGRTGYDNRREIMVKYIHKLSQGVENDAGDVGAAAPGAPGIFSSQPGHTHPA	60
Qy	46	GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH	79
Db	61	ASRDPVARTSLPTPAAPGAAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH	120
Qy	80	LTPPTARGFATVVEELFRDGVNNGRIVAPPEFGGVCMCVSNREMSPLVNIALWMTEY	139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 5

US-10-053-645A-21

; Sequence 21, Application US/10053645A

; Publication No. US20030176376A1

; GENERAL INFORMATION:

; APPLICANT: Robert E. Klem

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A

; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2

; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF

; FILE REFERENCE: 10412-022-999

; CURRENT APPLICATION NUMBER: US/10/053,645A

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: 60/263,244

; PRIOR FILING DATE: 2001-01-22

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-053-645A-21

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGPFISSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 6

US-10-387-961A-5

; Sequence 5, Application US/10387961A

; Publication No. US20030219474A1

; GENERAL INFORMATION:

; APPLICANT: TORMO, MAR

; APPLICANT: TARI, ANA M

; APPLICANT: LOPEZ-BERESTAIN, GABRIEL

; TITLE OF INVENTION: INHIBITION OF BCL-2 PROTEIN EXPRESSION BY LIPOSOMAL

; TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES

; FILE REFERENCE: UTXC:504USD1

; CURRENT APPLICATION NUMBER: US/10/387,961A

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: 08/726,211

; PRIOR FILING DATE: 1996-10-04

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-387-961A-5

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGPFISSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 7

US-10-003-632C-1

; Sequence 1, Application US/10003632C

; Publication No. US20040043028A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei

; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or

; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei

; FILE REFERENCE: CEN0269

; CURRENT APPLICATION NUMBER: US/10/003,632C

; CURRENT FILING DATE: 2001-11-02

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver 3.1

; SEQ ID NO 1

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-003-632C-1

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 7.2e-79;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGPFISSQPGHTPHPA 60

QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79

Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPPVVHLALROAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 139

Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFFFGGVMCVESVNREMSPLVDNIALMWTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166

Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 8

US-10-003-632C-3

; Sequence 3, Application US/10003632C

; Publication No. US20040043028A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Chichang; Ly, Celia; Moore, Gordon; Chi, Ximei

; TITLE OF INVENTION: Methods and Compositions for Enhanced Protein Expression and/or

; TITLE OF INVENTION: Cultured Cells Using Co-Transcription of a Bcl2 Encoding Nuclei

; FILE REFERENCE: CEN0269

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; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-3

Query Match      87.1%; Score 781.5; DB 4; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGDVGAAAPGAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 9
US-10-148-953A-1
; Sequence 1, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; FILE REFERENCE: 7398/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JP00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-953A-1

Query Match      87.1%; Score 781.5; DB 4; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGDVGAAAPGAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 166

; CURRENT APPLICATION NUMBER: US/10/003,632C
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-632C-3

Query Match      87.1%; Score 781.5; DB 4; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGDVGAAAPGAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 10
US-10-825-282-46
; Sequence 46, Application US/10825282
; Publication No. US20040224389A1
; GENERAL INFORMATION:
; APPLICANT: 3921-1-1-1
; TITLE OF INVENTION: VIRAL VECTORS ENCODING APOPTOSIS-INDUCING PROTEINS AND
; FILE REFERENCE: 3921-1-1-1
; CURRENT APPLICATION NUMBER: US/10/825,282
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/456,357
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: 60/134,416
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 09/087,195
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 08/378,507
; PRIOR FILING DATE: 1995-01-26
; PRIOR APPLICATION NUMBER: 08/250,478
; PRIOR FILING DATE: 1994-05-27
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-825-282-46

Query Match      87.1%; Score 781.5; DB 5; Length 239;
Best Local Similarity 73.4%; Pred. No. 7.2e-79;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHVKLSQRGYEWDAAGDVGAAAPGAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVPHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFPEFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 11
US-10-961-458-21
; Sequence 21, Application US/10961458
; Publication No. US20050170377A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: REGULATION OF BCL-2 GENE EXPRESSION
; FILE REFERENCE: 04040/1200990-US7
; CURRENT APPLICATION NUMBER: US/10/961,458
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US/10/961,458
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/375,514
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 09/080,285
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: US 08/465,485
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/124,256
; PRIOR FILING DATE: 1993-09-20
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; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutant Bcl-2
; OTHER INFORMATION: Gene, D34A
US-10-297-321-2
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Query Match      86.8%; Score 778.5; DB 4; Length 239;
Best Local Similarity 74.4%; Pred. No. 1.6e-78;
Matches 154; Conservative 2; Mismatches 10; Indels 41; Gaps 3;

Qy 1 MAHAGRTGYDNRREIVMKYIHVKLSQRYGWDAG-----DVEENRTBAPE 33
Db 1 MAHAGRTGYDNRREIVMKYIHVKLSQRYGWDAGVGAAPGAAAPAGIFSSQPGHTHPA 60

Qy 34 ---DDVEEN---RTEAPEGTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSLQTPAAPGAAAGPALSPPVPVHLLRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 180

Qy 140 LNRHLHTWIQDNGGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPMSR 207
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RESULT 15
US-10-148-953A-5
; Sequence 5, Application US/10148953A
; Publication No. US20040053228A1
; GENERAL INFORMATION:
; APPLICANT: SHIBAZAKI, FUTOSHI
; APPLICANT: KUMA, HIDEKAZU
; TITLE OF INVENTION: APOPTOSIS-INHIBITING POLYPEPTIDES, GENES AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING SAME, AND COMPOSITIONS CONTAINING THEM
; FILE REFERENCE: 7388/73088
; CURRENT APPLICATION NUMBER: US/10/148,953A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/JF00/08667
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: JP 11/350427
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: modified Bcl-2 protein
US-10-148-953A-5
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Query Match      86.7%; Score 777.5; DB 4; Length 239;
Best Local Similarity 72.9%; Pred. No. 2e-78;
Matches 151; Conservative 2; Mismatches 13; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNRREIVMKYIHVKLSQRYGWDAGD-----DVEENRTBAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHVKLSQRYGWDAGVGAAPGAAAPAGIFSSQPGHTHPA 60

Qy 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSLQTPAAPGAAAGPALSPPVPVHLLRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 139
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Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFEFEGGVMCVSVNREMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPMSR 207

Search completed: December 30, 2006, 12:29:38
Job time : 182 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:12:56 ; Search time 50 Seconds  
(without alignments)  
290.602 Million cell updates

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNREIVMKYIH.....WIQDNGGWDAFVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Minimum DB seq length: 0
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Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Minimum Match 08

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum March 100%  
Listing first 45 summaries

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1: /EMC_Celerra_SIDS3/ptodata/2/iaa/3_COMB.per:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.per:*
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4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pcp.\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE COMB.pep:\*

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7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	781.5	87.1	239	1	US-08-333-565-51
2	781.5	87.1	239	1	US-08-248-819A-12
3	781.5	87.1	239	1	US-08-690-095-4
4	781.5	87.1	239	1	US-08-465-485A-21
5	781.5	87.1	239	1	US-08-661-479-51
6	781.5	87.1	239	1	US-08-365-486A-15
7	781.5	87.1	239	1	US-08-337-646A-12
8	781.5	87.1	239	2	US-09-113-789-4
9	781.5	87.1	239	2	US-09-080-285-21
10	781.5	87.1	239	2	US-08-927-325-12
11	781.5	87.1	239	2	US-08-880-342-15
12	781.5	87.1	239	2	US-09-234-186-8
13	781.5	87.1	239	2	US-09-724-426-20
14	781.5	87.1	239	2	US-09-724-426-21
15	781.5	87.1	239	2	US-09-233-527-8
16	781.5	87.1	239	2	US-09-724-425-21
17	781.5	87.1	239	2	US-09-993-420A-8
18	781.5	87.1	239	2	US-10-003-632C-1
19	781.5	87.1	239	2	US-10-003-632C-3
20	781.5	87.1	239	2	US-08-726-211-5
21	781.5	87.1	239	3	US-09-375-514B-21
22	781.5	87.1	239	5	PCR-US93-05651-5
23	781.5	87.1	239	7	5459231-2
24	781.5	87.1	239	7	5506344-2
25	771.5	86.0	239	1	US-08-405-702A-12
26	769.5	85.8	239	1	US-08-115-208C-10
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28	769.5	85.8	239	1	US-08-115-208C-10
29	769.5	85.8	239	1	US-08-115-208C-10
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62	769.5	85.8	239	1	US-08-115-208C-10</

27	769.5	85.8	239	1	US-08-248-819A-10	Sequence 10, Appl
28	769.5	85.8	239	1	US-08-337-646A-10	Sequence 10, Appl
29	769.5	85.8	239	1	US-08-856-531-10	Sequence 10, Appl
30	769.5	85.8	239	1	US-08-856-034-10	Sequence 10, Appl
31	769.5	85.8	239	1	US-09-137-048-8	Sequence 8, Appl
32	769.5	85.8	239	2	US-08-927-326-10	Sequence 10, Appl
33	769.5	85.8	239	2	US-09-379-820A-10	Sequence 10, Appl
34	769.5	85.8	239	2	US-10-003-532C-10	Sequence 10, Appl
35	769.5	85.8	239	2	US-10-003-632C-13	Sequence 13, Appl
36	763.5	85.1	239	1	US-08-607-269-20	Sequence 20, Appl
37	763.5	85.1	239	1	US-08-471-058-12	Sequence 12, Appl
38	763.5	85.1	239	2	US-08-471-057-12	Sequence 12, Appl
39	763.5	85.1	239	2	US-08-470-865-12	Sequence 12, Appl
40	763.5	85.1	239	2	US-09-155-327G-11	Sequence 11, Appl
41	763.5	85.1	239	2	US-09-633-200-12	Sequence 12, Appl
42	763.5	85.1	239	5	FCT-US95-04600-20	Sequence 20, Appl
43	763	85.1	232	1	US-08-408-095-17	Sequence 17, Appl
44	761	84.8	232	1	US-08-408-095-18	Sequence 18, Appl
45	759	84.6	236	1	US-08-607-269-21	Sequence 21, Appl

## ALIGNMENTS

RECORD 1  
US-08-333-565-51  
Sequence 51, Application US/08333565  
Patent No. 562852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565

Query Match 87.1%: Score 781.5: DB 1: Length 239:

Query Match	87.1%;	Score /81.3;	DB
Best Local Similarity	73.4%;	Pred No	1e-85.

BEST LOCAL SIMILARITY 73.4%; F1ED: NO. 1E-83;  
Matches 152: Conservative 2: Mismatches

Matches 152; conservative 2; mismatches

1 MAHAGRTGYDNREI VMKYIHYKLSORGYEWDAGD--

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

1 MAHAGRTGYDNREIVMKYIHYKLSORGYEWDAGDVG

[illegible]

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Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPGAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 2
US-08-248-819A-12
; Sequence 12, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-248-819A-12

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPGIFSSQPGHTHPA 60
Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPGAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 4
US-08-465-485A-21
; Sequence 21, Application US/08465485A
; Patent No. 5831066
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Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 3
US-08-690-095-4
; Sequence 4, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,095
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0110 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 179367
US-08-690-095-4

Query Match 87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPGIFSSQPGHTHPA 60
Qy 46 CTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTTPAAPGAAGPALSPPVPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120
Qy 80 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNNGRIIVAFPEFGGVMCVESVNRMSPLVDNIALWMTEY 180
Qy 140 LNRHLHTWIQDNGWDADFVELYGPMSR 166
Db 181 LNRHLHTWIQDNGWDADFVELYGPMSR 207

RESULT 4
US-08-465-485A-21
; Sequence 21, Application US/08465485A
; Patent No. 5831066
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GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:  
FILING DATE: 21-FEB-1992  
APPLICATION NUMBER: US 07/840,716

PRIOR APPLICATION DATA:  
FILING DATE: 22-DEC-1988  
APPLICATION NUMBER: US 07/288,692

ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid

TOPOLOGY: linear,  
MOLECULE TYPE: protein  
US-08-465-485A-21

Query Match 87.1%; Score 781.5; DB 1; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDAGDVGAAAPGAPAGPFISSQPGHTPHFA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFATVVEELFRDGVNWRGRIVAFPFEGGVMCVESVNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNWRGRIVAFPFEGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 5  
US-08-661-479-51  
Sequence 51, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15726A-000700  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-661-479-51

Query Match 87.1%; Score 781.5; DB 1; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYGWDAGDVGAAAPGAPAGPFISSQPGHTPHFA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LTPFTARGFATVVEELFRDGVNWRGRIVAFPFEGGVMCVESVNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNWRGRIVAFPFEGGVMCVESVNREMSPLVDNIALWMTEY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 6  
US-08-365-486A-15  
Sequence 15, Application US/08365486A  
Patent No. 5834306  
GENERAL INFORMATION:  
APPLICANT: Webster, Keith A.  
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated  
TITLE OF INVENTION: Therapeutic Constructs  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA

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; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,486A
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-365-486A-15

Query Match      87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSLQTPAAPGAAAGPALSPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVCMVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVCMVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPSMR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPSMR 207

RESULT 7
US-08-337-646A-12
; Sequence 12, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
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; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-337-646A-12

Query Match      87.1%; Score 781.5; DB 1; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAGD-----DVEENRTEAPE 45
DB 1 MAHAGRTGYDNREIVMKYIHYKLSQGYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
DB 61 ASRDPVARTSLQTPAAPGAAAGPALSPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVCMVESVNREMSPLVDNIALWMTEY 139
DB 121 LTPFTARGRFATVVEELFRDGVNMGRIIVAFEFEGGVCMVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGWDADFVELYGPSMR 166
DB 181 LNRHLHTWIQDNGWDADFVELYGPSMR 207

RESULT 8
US-09-113-789-4
; Sequence 4, Application US/09113789
; Patent No. 6034219
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,789
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/690,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0110 US
```

TELECOMMUNICATION INFORMATION:  
NAME: Fortney, Andrew D.  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 179367  
US-09-113-789-4

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHDA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVYVHLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 139  
DB 121 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 9  
US-09-080-285-21  
Sequence 21, Application US/09080285  
Patent No. 6040181  
GENERAL INFORMATION:  
APPLICANT: Reed, John  
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Hwy., Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/080,285  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,485  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/124,256  
FILING DATE: 20-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/840,716  
FILING DATE: 21-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/288,692  
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:  
NAME: Fortney, Andrew D.  
REGISTRATION NUMBER: 34,600  
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (408) 436-2070  
TELEFAX: (408) 436-2075  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-080-285-21

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 1e-85;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;  
QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHDA 60  
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVYVHLALROAGDDFSRRYRGDFAEMSSQLH 120  
QY 80 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 139  
DB 121 LPTFTARGFATVVEELFRDGVNMGRIVAFFBFGGVMCVESVNREMSPLVDNIALMWTY 180  
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 10  
US-08-927-326-12  
Sequence 12, Application US/08927326  
Patent No. 6184202  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: CELL DEATH REGULATORS  
NUMBER OF SEQUENCES: 78  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/927,326  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/337,646  
FILING DATE: 10-NOV-1994  
APPLICATION NUMBER: US 08/248,819  
FILING DATE: 25-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/112,208  
FILING DATE: 26-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000620  
TELECOMMUNICATION INFORMATION:

```
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDEDNESS: single
MOLECULE TYPE: peptide
US-08-927-326-12

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
D 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
D 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
D 121 LTPFTARGRATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLTWIQDNGWDADFVELYGFMSR 166
D 181 LNRHLTWIQDNGWDADFVELYGFMSR 207

RESULT 11
US-08-880-342-15
Sequence 15, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Dehlinger & Associates
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-880-342-15

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
D 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
D 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
D 121 LTPFTARGRATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180
QY 140 LNRHLTWIQDNGWDADFVELYGFMSR 166
D 181 LNRHLTWIQDNGWDADFVELYGFMSR 207

RESULT 12
US-09-234-186-8
Sequence 8, Application US/09234186
Patent No. 6312947
GENERAL INFORMATION:
APPLICANT: Horvitz, H. Robert
APPLICANT: Hengartner, Michael
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 01997/201005
CURRENT APPLICATION NUMBER: US/09/234,186
CURRENT FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: 07/898,933
EARLIER FILING DATE: 1992-06-12
EARLIER APPLICATION NUMBER: 07/927,681
EARLIER FILING DATE: 1992-08-10
EARLIER APPLICATION NUMBER: 08/288,295
EARLIER FILING DATE: 1994-08-10
EARLIER APPLICATION NUMBER: 08/801,248
EARLIER FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-234-186-8

Query Match      87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
D 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAAPAGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
D 61 ASRDPVARTSPLQTPAAPGAAAGPALSPPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139
D 181 LNRHLTWIQDNGWDADFVELYGFMSR 207
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Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDADFVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPSMR 207

RESULT 13
US-09-724-426-20
; Sequence 21, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-426-20

Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPPHA 60
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTPAAGAAAGPALSPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDADFVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPSMR 207

RESULT 14
US-09-724-426-21
; Sequence 21, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-426-21

Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPPHA 60
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79
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Db 61 ASRDPVARTSPLOTPAAGAAAGPALSPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDADFVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPSMR 207

RESULT 15
US-09-233-527-8
; Sequence 8, Application US/09233527
; Patent No. 6465617
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hengartner, Michael
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF A
; TITLE OF INVENTION: GENE WHICH PROTECTS CELLS FROM PROGRAMMED CELL DEATH AND
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: 01997/201004
; CURRENT APPLICATION NUMBER: US/09/233,527
; CURRENT FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 07/898,933
; PRIOR FILING DATE: 1992-06-12
; PRIOR APPLICATION NUMBER: 07/927,681
; PRIOR FILING DATE: 1992-08-10
; PRIOR APPLICATION NUMBER: 08/288,295
; PRIOR FILING DATE: 1994-08-10
; PRIOR APPLICATION NUMBER: 08/801,248
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-233-527-8

Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 1e-85;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45
Db 1 MAHAGRTGYDNRREIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPPHA 60
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLOTPAAGAAAGPALSPVPPVHLLALROAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGRFATVVEELFRDGVNMGRIVAFFPFGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDADFVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDADFVELYGPSMR 207

Search completed: December 30, 2006, 12:14:19
Job time : 51 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2006, 12:03:31 ; Search time 199 Seconds  
(without alignments)  
381.397 Million cell updates/sec

Title: US-09-716-395-2

Perfect score: 897

Sequence: 1 MAHAGRTGYDNRNIVMKYIH.....WIQDNGWDFAVELYGPSMR 166

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_8:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*  
9: Geneseq2005s:\*  
10: Geneseq2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	897	100.0	166	5	ABG78476 Human Bcl
2	781.5	87.1	239	1	ABP80987 Sequence
3	781.5	87.1	239	2	AAR42312 Bcl-2 onc
4	781.5	87.1	239	2	AAR70331 Human bcl
5	781.5	87.1	239	2	AAR71404 Human bcl
6	781.5	87.1	239	2	AAR71404 Human bcl
7	781.5	87.1	239	2	AAR7812 Human B
8	781.5	87.1	239	4	AAG64035 Human Bcl
9	781.5	87.1	239	4	AB74129 Human bcl
10	781.5	87.1	239	5	ABG78477 Human Bcl
11	781.5	87.1	239	5	ABG78477 Human Bcl
12	781.5	87.1	239	5	ABG78477 Human Bcl
13	781.5	87.1	239	5	ABG78477 Human Bcl
14	781.5	87.1	239	5	ABG78477 Human Bcl
15	781.5	87.1	239	5	ABG78477 Human Bcl
16	781.5	87.1	239	6	ABG78477 Human Bcl
17	781.5	87.1	239	6	ABG78477 Human Bcl
18	781.5	87.1	239	6	ABG78477 Human Bcl
19	781.5	87.1	239	7	ABG78477 Human Bcl
20	781.5	87.1	239	8	ADL69723 Human Bcl
21	781.5	87.1	239	8	ADL69723 Human Bcl
22	781.5	87.1	239	8	ADL69721 Human Bcl
23	781.5	87.1	239	8	ADU22905 Human apo

#### ALIGNMENTS

##### RESULT 1

ABG78476

ID ABG78476 standard; protein; 166 AA.

XX AC ABG78476;

XX DT 15-NOV-2002 (first entry)

XX DE Human Bcl2 mutant protein.

XX KW Human; Bcl2; BclX1; programmed cell death; apoptosis; mutant; mtein.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200240530-A2..

XX PD 23-MAY-2002.

XX PF 15-NOV-2001; 2001WO-US045693.

XX PR 20-NOV-2000; 2000US-00716395.

XX PA (ABBO ) ABBOTT LAB.

XX PI Fesik SW, Petros AM, Yoon H, Nettlesheim DG;

XX DR WPI; 2002-490141/52.

XX PT New mutant Bcl-2 proteins derived from a wild type human Bcl-2 protein, useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis.

XX PS Claim 8; Page 20; 36pp; English.

XX CC This invention relates to a novel mutant protein which is derived from a wild type human Bcl-2 protein. The mutant is created by replacing a sequence of amino acid residues comprising a flexible loop from the wild type Bcl-2 protein with an amino acid sequence comprising at least two acidic amino acids. The mutant Bcl-2 protein comprises a 166 residue shown in the specification. The invention also comprises an assay for identifying substances that bind to the Bcl-2 protein. The protein sequences of the invention are useful in biological assays to identify substances that block the ability of Bcl-2 to inhibit programmed cell death or apoptosis. The present sequence represents a human Bcl2 mutant protein used in the invention

24 781.5 87.1 239 9 ADW13850 Human bcl  
25 781.5 87.1 272 2 AAY21120 Human bcl  
26 778.5 86.8 239 2 AAR47344 Human onc  
27 778.5 86.8 239 4 AAG64036 Human Bcl  
28 778.5 86.8 239 4 AAG64038 Human Bcl  
29 778.5 86.8 239 5 ABB05227 Human D34  
30 778.5 86.8 239 7 ADF28076 Mutant Bc  
31 777.5 86.7 239 4 AAG64039 Human Bcl  
32 775.5 86.5 239 4 AAG64037 Human Bcl  
33 771.5 86.0 239 2 AAW02383 Human Bcl  
34 769.5 85.8 239 2 AAW87810 A human B  
35 769.5 85.8 239 4 AAB35130 Human Bcl  
36 769.5 85.8 239 4 AAB74127 Human Bcl  
37 769.5 85.8 239 5 ABG78479 Human Bcl  
38 769.5 85.8 239 5 ABG78478 Human Bcl  
39 769.5 85.8 239 5 AAU76553 Human Bcl  
40 769.5 85.8 239 6 AAE37661 Human Bcl  
41 769.5 85.8 239 6 AAE37658 Bcl2 rela  
42 769.5 85.8 239 7 ADD45440 Human Pro  
43 769.5 85.8 239 7 ADF60831 Human apo  
44 769.5 85.8 239 7 ADI63113 Human apo  
45 769.5 85.8 239 8 ADJ66631 Bcl-2 pro

XX	SQ	Sequence 166 AA;
	Query Match	100.0%; Score 897; DB 5; Length 166;
	Best Local Similarity	100.0%; Pred. No. 8.4e-96;
	Matches 166; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MAHAGRTGYDNRREIVMKYIHYKLSQRGYEWADGDDVEENRTEAPEGTSESVVHLALROAG 60
DB	1	MAHAGRTGYDNRREIVMKYIHYKLSQRGYEWADGDDVEENRTEAPEGTSESVVHLALROAG 60
QY	61	DDFSRRRYRGDPFAENSSQLHLTPFTARGRFATVVVELPRDGVNNGRIVAFFPFGVMCVES 120
DB	61	DDFSRRRYRGDPFAENSSQLHLTPFTARGRFATVVVELPRDGVNNGRIVAFFPFGVMCVES 120
QY	121	VNREMSPLVDNIALLWMTLEYLNRHLHTWIQDNGWDADFELYGPSMR 166
DB	121	VNREMSPLVDNIALLWMTLEYLNRHLHTWIQDNGWDADFELYGPSMR 166
RESULT 2		
AAP80987	ID	AAP80987 standard; protein; 239 AA.
XX	AC	AAP80987;
XX	DT	17-DEC-1990 (first entry)
XX	DE	Sequence of bcl-2-alpha encoded by sequence of bcl-2 cDNA corresp. to the
XX	DE	5.5 kb transcript.
XX	KW	B-cell neoplasm; diagnosis; follicular lymphomas.
XX	OS	Homo sapiens.
XX	PN	EP252685-A.
XX	PD	13-JAN-1988.
XX	PJ	02-JUL-1987; 87EP-00305863.
XX	PR	09-JUL-1986; 86US-00883687.
XX	PA	(WIST-) WISTAR CORP.
XX	PI	Tsujiimoto Y, Croce CM;
XX	DR	WFI; 1988-008633/02.
XX	DR	N-PSDB; AAN81292.
XX	PT	Detection of B-cell neoplasms - by extn. of proteins or RNA from B-cells
XX	PT	and quantitation using specific antibody or DNA probe.
XX	PS	Claim 12; Fig 2A-2D; 23pp; English.
CC	CC	A human bcl-2 gene substantially free of introns is claimed. Also claimed
CC	CC	is a substantially pure preparation of a protein having an N-terminal end
CC	CC	encoded by the first exon of the human bcl-2 gene wherein said protein is
CC	CC	bcl-2-alpha having about 239 (AAP80987) or 205 (AAD80988) AA residues. B-
CC	CC	cell neoplasms which are associated with t(14;18) chromosome
CC	CC	translocations cause an increase in expression of both the mRNA and the
CC	CC	protein prods. of the bcl-2 gene. This is used to detect B-cell neoplasms
CC	CC	including follicular lymphomas as well as other lymphomas. Bacterial
CC	CC	isolates available as ATCC 67147 and 67148 can be used to express bcl-2
CC	CC	gene products alpha (AAN81292) and beta (AAN91293) resp. in bacteria
XX	XX	Sequence 239 AA;
	Query Match	87.1%; Score 781.5; DB 1; Length 239;
	Best Local Similarity	73.4%; Pred. No. 4e-82;
	Matches 152; Conservative	2; Mismatches 12; Indels 41; Gaps 2
OY	1	MAHAGRTGYDNRREIVMKYIHYKLSQRGYEWADG-----DYENRTEAPE 45

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Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVVLALROAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGPATVVEELFRDGVNNGRIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGPATVVEELFRDGVNNGRIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 4
AAR70331
ID AAR70331 standard; protein; 239 AA.
XX
AC AAR70331;
XX
DT 25-MAR-2003 (revised)
DT 27-SEP-1995 (first entry)
XX
DE Human bcl-2 protein.
XX
KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW Chemoresistance.
XX
OS Homo sapiens.
XX
PN WO9508350-A1.
XX
PD 30-MAR-1995.
XX
PF 20-SEP-1994; 94WO-US010725.
XX
PR 20-SEP-1993; 93US-00124256.
XX
PA (REED/J) REED J C.
XX
PI Reed JC;
XX
DR WPI; 1995-139394/18.
XX
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human
PT solid tumours, esp. breast cancer.
XX
PS Disclosure; Page 71-72; 108pp; English.
XX
CC The human bcl-2 gene encodes a 25 kDa protein (AAR70331). Antisense
CC oligonucleotides have been designed to bind sites in mRNA transcribed
CC from the bcl-2 gene, thereby reducing expression of the bcl-2 protein and
CC inducing cell death in certain cancer cells. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 239 AA;
Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;
QY 1 MAHAGRTGVDNRIRVIMKYIHYKLSQRYEWDAGD-----DVENRTEAPE 45
Db 1 MAHAGRTGVDNRIRVIMKYIHYKLSQRYEWDAGDVGGAAPGAPGIFSSQPGHTPHEA 60
QY 46 GTES-----EVVHLALROAGDDFSRRYRGDFAEMSSQLH 79
Db 61 ASRDPVARTSPLQTPAAPGAAGPALSPVPVVLALROAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGPATVVEELFRDGVNNGRIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGPATVVEELFRDGVNNGRIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207
```

```
RESULT 5
AAR71404
ID AAR71404 standard; protein; 239 AA.
XX
AC AAR71404;
XX
DT 25-MAR-2003 (revised)
DT 30-OCT-1995 (first entry)
XX
DE Human bcl-2 alpha protein.
XX
KW Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
KW proliferation; cell cycle progression; Bax; apoptotic cell death;
KW apoptosis; cytokine; death repressor; BHL; BH2; cancer therapy;
KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
KW ischaemic cell death.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 136..155
FT FT /label= BH1 domain
FT FT /note= "Represents Bax binding site"
FT FT 187..202
FT FT /label= BH2 domain
FT FT /note= "Represents Bax binding site"
XX
PN WO9505750-A1.
XX
PD 02-MAR-1995.
XX
PF 24-AUG-1994; 94WO-US009701.
XX
PR 26-AUG-1993; 93US-00112208.
PR 25-MAY-1994; 94US-00248819.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI; 1995-106605/14.
XX
PT Methods for producing and identifying mutant bcl-2 proteins - that lack
PT death repressor activity and/or lacks binding to Bax.
XX
PS Disclosure; Page 39; 133pp; English.
XX
CC The sequences given in AAR71404-05 represent the human bcl-2 alpha and
CC beta proteins respectively. bcl-2 is encoded by a proto-oncogene and is
CC capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2
CC is a 26 kD membrane-associated cytoplasmic protein and is thought to
CC function by enhancing the survival of hematopoietic cells of B and T
CC origins rather than directly promoting proliferation of these cell types.
CC bcl-2 has not been shown to directly promote cell cycle progression nor
CC does it necessarily alter the dose response to limiting concentrations of
CC IL-3. bcl-2 has been shown to form heterodimers with a 21 kD protein,
CC Bax. Overexpressed Bax accelerates apoptotic cell death induced by
CC cytokine deprivation in an IL-3 dependent cell line, and it also acts to
CC counter the death repressor activity of bcl-2. Therefore, the ratio
CC between bcl-2 and Bax determines cell survival or death following an
CC apoptotic stimulus. The invention gives a mutant form of bcl-2 in which
CC there is at least one amino acid substitution or deletion in the BHL or
CC BH2 domains. This makes the mutant protein substantially incapable of
CC binding Bax and/or incapable of death repressor activity. Down regulation
CC of bcl-2 is useful in cancer therapy, controlling hyperplasias and
CC eliminating self-reactive clones in autoimmunity by favouring death
CC effector molecules. Up regulating bcl-2 is beneficial in treatment and
CC diagnosis of immunodeficiency diseases, including AIDS and
CC neurodegenerative and ischaemic cell death. (Updated on 25-MAR-2003 to
CC correct PN field.)
```

```
XX SQ Sequence 239 AA;
Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGRTGYDNREIVMKYIHYKLSQRCYEWDAKD-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79
Db 1 MAHAGRTGYDNREIVMKYIHYKLSQRCYEWDAKDVGAAAPGAPGIFSSQPGHTHPA 60
QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 120
Db 61 ASRDPVARTSPLQTTPAAPGAAAGPALSPVPVPPVHLALRQAGDDFSRRYRGDFAEMSSQLH 120
QY 80 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 139
Db 121 LTPFTARGFATVVEELFRDGVNMGRIIVAFEFEGGVMCVESVNREMSPLVDNIALWMTEY 180
QY 140 LNRHLHTWIQDNGGWDFAVELYGPMSR 166
Db 181 LNRHLHTWIQDNGGWDFAVELYGPMSR 207

RESULT 7
AAW87812
ID AAW87812 standard; protein; 239 AA.
XX AC AAW87812;
XX AC
XX DT 10-MAR-1999 (first entry)
XX DE A human Bcl-2-alpha protein.
XX KW Human; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
XX KW bcl-2-related function; apoptosis; dimer; Bcl-xL; Mcl-1; A1.
XX OS Homo sapiens.
XX PN US5856171-A.
XX PD 05-JAN-1999.
XX PF 10-NOV-1994; 94US-00337646.
XX PR 26-AUG-1993; 93US-00112208.
XX PR 25-MAY-1994; 94US-00248819.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Korsemeyer SJ;
XX DR WPI; 1999-105119/09.
XX PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX PS identifying modulators of bcl-2 function.
XX PS Disclosure; Col 29; 105pp; English.
XX CC The present sequence represents a human Bcl-2-alpha protein. The
XX CC specification also describes Bcl-2 associated proteins designated Bax.
XX CC The Bax protein is used in a composition which comprises a bcl-2 family
XX CC member polypeptide, a naturally occurring Bax polypeptide and an antibody
XX CC that binds to the Bax polypeptide. The specification also describes a
XX CC composition comprising a hybrid protein comprising an activator domain of
XX CC a transcriptional activator protein and a bcl-2 family member having a
XX CC BHL domain and a BH2 domain; another hybrid protein comprising a DNA-
XX CC binding domain of the transcriptional activator protein and a second bcl-
XX CC 2 family member having a BHL domain and a BH2 domain; and a reporter gene
XX CC linked to a transcriptional regulatory element whose transcriptional
XX CC activity is dependent on the presence or absence of a dimer of the two
XX CC hybrid proteins. The bcl-2 family members are selected from naturally
XX CC occurring Bcl-2, Bcl-xL, Bax, Mcl-1, A1, fragments thereof, and mutants
XX CC having a mutation in the BHL and/or BH2 domain that alters intermolecular
XX CC binding of the two bcl-2 family members. The compositions are used to
XX CC identify modulators of bcl-2-related function, e.g. substances that
XX CC inhibit binding of Bax to bcl-2, which would be potentially useful as
XX CC drugs for modulating apoptosis
XX SQ Sequence 239 AA;

RESULT 6
AAW40217
ID AAW40217 standard; peptide; 239 AA.
XX AC AAW40217;
XX DT 07-JUL-1998 (first entry)
XX DE Human bcl-2.
XX KW TMAH; apoptosis; osteoarthritis; c-type lectin; A1 family; diagnosis;
XX KW treatment.
XX OS Homo sapiens.
XX PN WO9804585-A2.
XX PD 05-FEB-1998.
XX PF 22-JUL-1997; 97WO-US013077.
XX PR 31-JUL-1996; 96US-00690095.
XX PA (INCY-) INCYTE PHARM INC.
XX PI Hillman JL, Au-Young J, Goli SK;
XX DR WPI; 1998-130617/12.
XX PT Human macrophage antigen - used for decreasing apoptosis associated with
XX PS osteoarthritis.
XX PS Disclosure; Page 43; 58pp; English.
XX CC The human bcl-2 peptide is one of a group of peptides with which the
XX CC human macrophage antigen (TMAH) (AAW40215) has 20% homology. The homology
XX CC which TMAH shares with the other A1 family members includes conserved
XX CC residues at F27, P35, R139, W139, F146 AND W214. The structural homology
XX CC between the mammalian A1 and C-type lectins and TMAH provides information
XX CC on the structural and physical properties of both the TMAH gene and
XX CC protein. This is used in the development of TMAH as a diagnostic tool and
XX CC as a method of treating diseases associated with expression of TMAH
XX SQ Sequence 239 AA;
Query Match 87.1%; Score 781.5; DB 2; Length 239;
Best Local Similarity 73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;
```

Query Match 87.1%; Score 781.5; DB 2; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45  
DB 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAPALSPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 8

AAG64035

ID AAG64035 standard; protein; 239 AA.

XX AC

AC AAG64035;

XX AC

DT 10-SEP-2001 (first entry)

XX DT

XX DE Human Bcl-2 protein.

XX DE

KW Human; Bcl-2; gene therapy; apoptosis inhibitor; mutant.

XX KW

XX OS Homo sapiens.

XX OS

XX PN WO200142459-A1.

XX PN

XX PD 14-JUN-2001.

XX PD

XX PF 07-DEC-2000; 2000WO-JP008667.

XX PF

XX PR 09-DEC-1999; 99JP-00350427.

XX PR

XX PA (HISM ) HISAMITSU PHARM CO LTD.

XX PA

XX PI Shibasaki F, Kuma H;

XX PI

XX PS WPI; 2001-381681/40.

XX PS

XX DR N-PSDB; AAH45293.

XX DR

XX PT New apoptosis inhibitors, useful for treating apoptosis related

XX PT

XX PS disorders.

XX PS

XX CC Claim 1; Page 29-30; 43pp; Japanese.

XX CC

XX CC The invention relates to an apoptosis inhibitor comprising the amino acid

XX CC

XX CC sequence of Bcl-2 protein in which at least one serine residue is

XX CC

XX CC substituted by alanine or aspartic acid. The protein has increased

XX CC

XX CC apoptosis inhibitory activity compared with the wild type Bcl-2 protein.

XX CC

XX CC The mutated Bcl-2 protein is useful in the treatment of disorders caused

XX CC

XX CC by apoptosis. The present sequence is the wild type human Bcl-2 protein

XX CC

XX SQ Sequence 239 AA;

XX SQ

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 4e-82;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

DB 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHPA 60

QY 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
DB 61 ASRDPVARTSPLQTPAAPGAAAPALSPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLH 120

QY 80 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 139  
DB 121 LTPFTARGFATVVEELFRDGVNMGRIVAFFFGVCMCVSNREMSPLVDNIALWMTEY 180

QY 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
DB 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

## RESULT 9

AAB74129

ID AAB74129 standard; protein; 239 AA.

XX AC

AC AAB74129;

XX AC

DT 22-MAY-2001 (first entry)

XX DT

XX DE Human bcl-2alpha.

XX DE

XX KW Human; Bax; cytostatic; immunosuppressive; immunostimulant; infection;

XX KW

KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;

KW

KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

KW

KW myocardial infarction; traumatic brain injury; ischaemia; bcl-2alpha;

KW

KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

KW

XX lymphoproliferative disease; chromosome 18q21.3.

XX XX

OS Homo sapiens.

XX OS

XX PN US6184202-B1.

XX PN

XX PD 06-FEB-2001.

XX PD

XX PF 11-SEP-1997; 97US-00927326.

XX PF

XX XX 26-AUG-1993; 93US-00112208.

XX XX

XX PR 25-MAY-1994; 94US-00248819.

XX PR

XX PR 10-NOV-1994; 94US-00337646.

XX PR

XX PA (UNIW ) UNIV WASHINGTON.

XX PA

XX PI Korsmeyer SJ;

XX PI

XX XX WPI; 2001-256104/26.

XX XX

XX PT Modulating apoptosis of a cell, useful in maintaining homeostasis in

XX PT

XX PT adult tissues, or treating proliferative or autoimmune diseases,

XX PT

XX PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd

XX PT

XX PT bcl-2 associated X protein.

XX PT

XX PS Disclosure; Col 29-30; 105pp; English.

XX PS

XX XX The present invention relates to a method of modulating apoptosis of a

XX XX

XX CC cell. The method comprises administering to the cell an agent,

XX CC

XX CC comprising a BHL domain or BH2 domain, capable of modulating formation of

XX CC

XX CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL

XX CC

XX CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax

XX CC

XX CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially

XX CC

XX CC useful in cancer therapy, and treating autoimmunity, immunodeficiency

XX CC

XX CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,

XX CC

XX CC traumatic brain injury, neurodegenerative diseases, aging, ischaemia,

XX CC

XX CC toxemia, infection, hepatitis, transplant rejection, and

XX CC

XX CC lymphoproliferative diseases. The present sequence is human Bcl-2alpha,

XX CC

XX CC which was used in the method of the present invention. The human Bcl-2

XX CC

XX CC gene is located on chromosome 18q21.3

XX CC

XX SQ Sequence 239 AA;

XX SQ

Query Match 87.1%; Score 781.5; DB 4; Length 239;

Best Local Similarity 73.4%; Pred. No. 4e-82;

Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

QY 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGD-----DVEENRTEAPE 45

DB 1 MAHAGTGYDNRIVMKYIHYKLSQRYEWDAGDVGAAAPGAPGIFSSQPGHTPHPA 60





CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,  
CC for ex vivo bone marrow purging, for removing residual malignant cells  
CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,  
CC and for treating autoimmune disease  
XX  
SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVEENRTEAPE 45  
Db 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPA 60

Qy 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRATVVEELFRDGVNMGRIIVAFEFEGVMCVESVNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRATVVEELFRDGVNMGRIIVAFEFEGVMCVESVNREMSPLVDNIALWMTEY 180

Qy 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 14  
ABB78196  
ID ABB78196 standard; protein; 239 AA.  
AC ABB78196;  
XX  
XX 25-NOV-2002 (first entry)  
XX  
XX Amino acid sequence of human bcl-2.  
XX  
XX Antisense oligonucleotide; B cell lymphoma/leukemia-2 gene; bcl-2 gene;  
KW cancer; lymphoma; leukemia; chemotherapeutic agent; bone marrow purging;  
KW autoimmune disease.  
XX  
XX Homo sapiens.  
XX  
XX US6414134-B1.  
XX  
XX 02-JUL-2002.  
XX  
XX 28-NOV-2000; 2000US-00724426.  
XX  
XX 22-DEC-1988; 88US-00288692.  
PR 21-FEB-1992; 92US-00840716.  
PR 20-SEP-1993; 93US-00124256.  
PR 05-JUN-1995; 95US-00455485.  
PR 18-MAY-1998; 98US-00080285.  
PR 17-AUG-1999; 99US-00375514.  
XX  
XX (UYPE-) UNIV PENNSYLVANIA.  
XX  
XX Reed JC;  
XX  
XX WPI; 2002-641579/69.  
DR N-PSDB; ABQ78196.  
XX  
XX Novel antisense oligonucleotide complementary to B cell lymphoma/leukemia  
PT -2 mRNA, useful for inhibiting cancer cell growth, for treating  
PT autoimmune disorders, and for ex vivo bone marrow purging.  
XX  
XX Example 18; Col 37-40; 41pp; English.  
XX  
XX The present sequence represents B cell lymphoma/leukemia-2 (bcl-2). The  
CC specification describes antisense oligonucleotides complementary to B  
CC cell lymphoma/leukemia-2 (bcl-2) mRNA. The antisense oligonucleotide is

CC useful for inhibiting cancer cell (lymphoma or leukemia cells) growth,  
CC for increasing the sensitivity of cancer cells to cancer chemotherapeutic  
CC agents, or for inducing cancer cell death alone or in combination with  
CC any one or more cancer chemotherapeutic agents. It is also useful for  
CC reducing the bcl-2 gene expression or impairing bcl-2 protein function,  
CC for ex vivo bone marrow purging, for removing residual malignant cells  
CC from the bone marrow, for inhibiting cancer of neoplastic cell growth,  
CC and for treating autoimmune disease  
XX  
SQ Sequence 239 AA;

Query Match 87.1%; Score 781.5; DB 5; Length 239;  
Best Local Similarity 73.4%; Pred. No. 4e-82;  
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;

Qy 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGD-----DVEENRTEAPE 45  
Db 1 MAHAGRTGYDNREIVMKYIHVKLSQRYEWDAGDVGAAAPGAAAPGIFSSQPGHTHPA 60

Qy 46 GTES-----EVVHLALRQAGDDFSRRYRGDFAEMSSQLH 79  
Db 61 ASRDPVARTSPLQTPAAPGAAAGPALSPVPVHVALRQAGDDFSRRYRGDFAEMSSQLH 120

Qy 80 LTPFTARGRATVVEELFRDGVNMGRIIVAFEFEGVMCVESVNREMSPLVDNIALWMTEY 139  
Db 121 LTPFTARGRATVVEELFRDGVNMGRIIVAFEFEGVMCVESVNREMSPLVDNIALWMTEY 180

Qy 140 LNRHLHTWIQDNGGWDFAVELYGPSMR 166  
Db 181 LNRHLHTWIQDNGGWDFAVELYGPSMR 207

RESULT 15  
ABB75986  
ID ABB75986 standard; protein; 239 AA.  
XX  
XX ABB75986;  
XX  
XX 12-JUL-2002 (first entry)  
XX  
XX Protein sequence.  
XX  
XX B cell lymphoma/leukemia-2; bcl-2; oncogene; antisense; lymphoma;  
KW leukaemia; colon carcinoma; rectal carcinoma; pancreatic cancer;  
KW breast cancer; ovarian cancer; prostate cancer; renal cell carcinoma;  
KW hepatoma; bile duct carcinoma; choriocarcinoma; cervical cancer;  
KW testicular cancer; lung carcinoma; bladder carcinoma; melanoma;  
KW head and neck cancer; brain cancer; cytostatic; human; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO200217852-A2.  
XX  
XX 07-MAR-2002.  
XX  
XX 23-AUG-2001; 2001WO-US026414.  
XX  
XX 25-AUG-2000; 2000US-0227970P.  
PR 29-SEP-2000; 2000US-0237009P.  
PR 10-NOV-2000; 2000US-00709170.  
XX  
XX (GENT-) GENTA INC.  
PA  
XX Warrel RP, Klem RE, Fingert H;  
XX  
XX WPI; 2002-371796/40.  
DR N-PSDB; ABL54167.  
XX  
XX Treating or preventing cancer, tumors and carcinomas, comprises  
PT administering B cell lymphoma/leukemia-2 antisense oligonucleotide at  
PT high doses for short period for time with one or more cancer  
PT therapeutics.  
XX



Disclosure; Page 61; 64pp; English.

XX

The present invention is related to the use of a B cell lymphoma/leukaemia-2 (bcl-2) antisense oligonucleotide, particularly G3139 (see AB54148), to treat and prevent bcl-2 related disorders. Administration at high doses results in significant therapeutic responses, including low toxicity, high tolerance and prolonged survival. Administration at high doses for short periods of time (less than 14 days) also provides significant therapeutic responses in the treatment of cancer. The bcl-2 antisense oligomer may also be used to increase the sensitivity of a subject to cancer therapeutics, and in combination with hormone treatment or gene therapy. Conditions that may be treated or prevented include cancer of the haematopoietic system, skin, bone and soft tissue, reproductive system, genitourinary system, breast, endocrine system, brain, central nervous system, peripheral nervous system, kidney, lung, respiratory system, thorax, gastrointestinal and alimentary canal, lymph nodes, pancreas, hepatobiliary system, or cancer of unknown primary site, non-Hodgkin's lymphoma, Hodgkin's lymphoma, leukaemia, colon carcinoma, rectal carcinoma, pancreatic, breast, ovarian, prostate, cervical, testicular, head and neck or brain cancer, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, lung carcinoma, bladder carcinoma and melanoma (all claimed). Note: The present sequence is given in the Sequence Listing from the present invention but the Seq ID No. is not referred to within the specification

Sequence 239 AA;

Query Match	87.1%; Score 781.5; DB 5; Length 239;
Best Local Similarity	73.4%; Pred. No. 4e-82;
Matches 152; Conservative 2; Mismatches 12; Indels 41; Gaps 2;	
QY	1 MAHAGRTGYDNREIVMKYIHYKLSORSYGENDAGD-----DV EENRTEAPE 45 
Db	1 MAHAGRTGYDNREIVMKYIHYKLSORSYGENDAGDVGAAAPGCAAPAGIFSQPGHTHPA 60 
QY	46 GTES-----EVVHLALRQAQDDPSRRYRGDFAE MSSQLH 79    :
Db	61 ASRPDPVARTSPLQTPAAPGAAAGPALSPVPVPPVVHLALRQAQDDPSRRYRGDFAE MSSQLH 120 
QY	80 LTFPTTARGRATVVEELFRDGVNMGRIVAFFFGGVNCVSVNREMPLVDNTALWMTXY 139 
Db	121 LTFPTTARGRATVVEELFRDGVNMGRIVAFFFGGVNCVSVNREMPLVDNTALWMTXY 180 
QY	140 LNPHLHTWIQDNGGWDAFVELYGPSMR 166 
Db	181 LNPHLHTWIQDNGGWDAFVELYGPSMR 207 

Search completed: December 30, 2006, 12:07:32  
Job time : 202 secs

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